

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 144
<211> 6928
<212> DNA
<213> Homo sapiens

<400> 144
ggccggcggc cgtgcgcccc aggaccggc cggaaggctt ggcgcagtc aggatgagga 60
cagggtggcc gaccccttcg cccggccggg ggcttcctcgat gctgttttc tggtttttcg 120
attcggccgc gcccccttgc cggccgcata ttatggccccc caccatgcg catggaaactg 180
ggccggcaatg ctatcaaccgat ccgtatggat ggtatgttcg gatgtatgc agacgactgt 240
ggccgttggcc ctatattacc acatggcttaa atggatgttcg tttatgttc cttatgttc 300
gttgcatgtcc gtgtggggaaa ttgtggaccac actttctgtt cggcgcgtt cggatccgc 360
gggtctctggaa ggatggacat gcacacgcaa ttccaaatgtc cttatgttc atctgtatgc 420
gaggctcaga gaaacccgtt tggttggaccg ctatcatgtt gatctatacc agagatggaa 480
actttatggg gggatccgtt gatattccat tcttaattgtt tgggacttgg caccatataat 540
gcatttttgcc tggatggatc ttggggccat ggtgttgcac cttatgttc tggttttttt 600
ggggacaaatgg gggatccgtc tttaaggctt aaadacgggtt tgaaagataat tggttttttt 660
acggcagggtt tggatgttc tttatgttc attacagac ggtttttttt tgggaaaaaa 720
ttttatgttc atggatcaat caaggatgtt attatgttgat cttatgttc cttatgttc 780
taatcttcgtt taatggggaaa ggatggatgtt ttatgttgat cttatgttc cttatgttc 840
atccggcagac gggccatgtca cttatgttc ttatgttgat cttatgttc cttatgttc 900
atgtgtgttc tggttggaccg ttatgttc ttatgttgat cttatgttc cttatgttc 960
cattaatggcc facatggggat tttaacatgtt tggttggaccat cttatgttc cttatgttc 1020
cggctgtgtt gccaatataat gatgttgcgtt atctgtgtt aatggaaatgtt cttatgttc 1080
ggccggccaca tggccggatcc acggccatgtt tgatgttgat cttatgttc cttatgttc 1140
cagatgttgg tttttttttt ttatgttgat cttatgttc cttatgttc cttatgttc 1200
tagggctttaa gaaatcaaaac ataccaatcc ttatgttgat cttatgttc cttatgttc 1260
cttcaacata ttggatgttgat gggatccgtt ttatgttgat cttatgttc cttatgttc 1320
ttttctactt agggagatgtt gttttaggtggaa atttttttttt ttatgttgat cttatgttc 1380
atgtatggcc gggatggggaa aaaaactttttt ttatgttgat cttatgttc cttatgttc 1440
cagatgtgggg ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 1500
tttttgttggaa aacttgcattt ttatgttgat cttatgttc cttatgttc cttatgttc 1560
atttatgtggaa atttttttttt ttatgttgat cttatgttc cttatgttc cttatgttc 1620
tagatgtggaa atttatgttgat aatcttcaat aaaaactttttt ttatgttgat cttatgttc 1680
ttttccacttgg tggttggatggat gggatccgtt ttatgttgat cttatgttc cttatgttc 1740
gaaatctgtt gaaatctttttt ttatgttgat cttatgttc cttatgttc cttatgttc 1800
ggcaatgttgg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 1860
gttccgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 1920
ggggatgggggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 1980
ggccggccatgtt ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2040
ggccggccatgtt ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2100
ggccggccatgtt ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2160
ggccggccatgtt ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2220
ggccggccatgtt ttggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2280
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2340
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2400
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2460
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2520
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2580
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2640
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2700
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2760
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2820
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2880
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 2940
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3000
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3060
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3120
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3180
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3240
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3300
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3360
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3420
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3480
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3540
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3600
tttgcgttgggg gggatggggaa atttttttttt ttatgttgat cttatgttc cttatgttc 3660

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

ataggattctg gaaaacagt gattgcattc acaatcaacc aggtgttattt tgctactttt 3720
caggaatgtg gactgtaaaaa gaggtcaaac cagttgcacg tggtaaatgtt ccatcttcgt 3780
ttccaaatctc tccgtggata ccatttcaga caatgttcta ataaacaaga 3840
ataggcatat ggcaacaaca caggatggaa ttccatactaa atggcagaaa ctgaatccaa 3900
aatcacatat tcttgatattt cgagatgaaa aggagaataa ctttgttctt gaccaactgc 3960
tgttacticat ttatatgggt tcattgggtca tggtaggaat aactttataga aataattctc 4020
ttatgtgtt tgataagacc ccattgttcat atacacatgg gagagcaggaa agaccaacta 4080
ttaaaaatgtg gaagttttt gctggtttaa gtactgtcggg cttctggat attcaacactt 4140
ttaaaatgtt tgaaagcga gtttattttc accagcacag catcttgcgt tgtaaatgg 4200
aaatgttggt ctacaagaga aacataataa ctacactgcg acgtttatg ctatcatggaa 4260
atgggttattt cagttgttat caaaaaaaaagg taacatggta tgaagcattt aacatgtt 4320
cttcaaaatgg aggttacttgc gcaaggcgatc aaccaaaaaa tgccggatc tttctggaa 4380
atattgttaa agctgtatgg ttccactat ggggttgggt ctcaactgtc gatggaaatgg 4440
aatacaatgtt gatggatgtt gatggtagta cattttgtacta ttatccatgg aaaggcccaa 4500
catctcccttg aatattgtgtt ctcttggatc caaaaggaaac ttggaaacatg aatattgtca 4560
actcttggat ggtatgtgtt attttgtata aaccttacaaa atctttttttt cttgtccgc 4620
ttcalatctc atcaatgtt ccagcagca aagagaatgg gtcacgggtgg atccaggatca 4680
agggttactt ttacaatgtt gatccggatc tgccaggatc tttccaggccc aaaaatgtt 4740
gttccaaatctc tgatctactc gcaactatcg ttccatataa agatgttggat gagaataataat 4800
tttgtagcag agttgtatgg gaaaatataa acattttatc gaggtttttt ctggatgtt 4860
cttcaacatctc ttgttggatc ttcttggatgtt gtttagatgg atcagaatgtt atctttgtca 4920
aatggggaaa taaaatgttgg agttgtgtttt gaaatgttgg atcgttggat gttttttttt 4980
aaacttggaa aaaaatgttgg tttttttttt atcagatgtt gatgttggat aatgttgc 5040
tggggccctgt tttttttttt atcagatgtt tttttttttt atcagatgtt gatgttggat 5100
tggggccggat gttttttttt ttccatccaa ggccatggcc gttttttttt atcagatgtt tttttttttt 5160
cagttggatc tttttttttt ttccatccaa ggccatggcc gttttttttt atcagatgtt tttttttttt 5220
aaatttttttt aaaaatgttgg tttttttttt atcagatgtt gatgttggat tttttttttt 5280
aaatgttccca ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 5340
ttttttttttt ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 5400
tacaccctt attatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 5460
tgatcagttat ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 5520
tgatatattt aataatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 5580
agggttgcattc ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 5640
caaaatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 5700
cttggggaaaat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 5760
gttcccttcctt ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 5820
cgccctcccgat ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 5880
aacttgcaccat ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 5940
ggccaggctgt ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 6000
cttggggatcat ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 6060
agggttgcattc ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 6120
faataatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6180
tagtgcattttt cttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6240
agcgttgcattt ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 6300
actatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6360
tgatcagttat ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 6420
gaaatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6480
gatgttgcattc ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 6540
actttttttt tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6600
tttgacccatc tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6660
aatgttgcattt ttgttggatc ttatgttggat tttttttttt atcagatgtt gatgttggat 6720
tagatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6780
acatgttgcattc ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 6840
cttggatgttgc ttatgttggat tttttttttt atcagatgtt gatgttggat tttttttttt 6900
ttttttttttt tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6960
ttttttttttt tttttttttt atcagatgtt gatgttggat tttttttttt atcagatgtt gatgttggat 6928

```

<210> 145

<211> 1722

<212> PRT

<213> Homo sapiens

<400> 145

Met	Arg	Thr	Gly	Trp	Ala	Thr	Pro	Arg	Arg	Pro	Ala	Gly	Leu	Leu	Met
1				5						10				15	
Leu	Leu	Phe	Trp	Phe	Phe	Asp	Leu	Ala	Glu	Pro	Ser	Gly	Arg	Ala	Ala
		20							25				30		
Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Gly	Asn	Thr	Gly	Lys	Cys	Ile	Lys

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 35 40 45
 Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
 50 55 60
 Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
 65 70 75 80
 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
 85 90 95
 Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
 100 105 110
 His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
 115 120 125
 His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
 130 135 140
 Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
 145 150 155 160
 Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
 165 170 175
 Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
 180 185 190
 Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
 195 200 205
 Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
 210 215 220
 Gln Phe Gly Ser Cys Tyr Glu Phe Asn Thr Gln Thr Ala Leu Ser Trp
 225 230 235 240
 Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Lys Ser
 245 250 255
 Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
 260 265 270
 Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
 275 280 285
 Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
 290 295 300
 Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
 305 310 315 320
 Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
 325 330 335
 Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
 340 345 350
 Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
 355 360 365
 Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
 370 375 380
 Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
 385 390 395 400
 Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
 405 410 415
 Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
 420 425 430
 Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
 435 440 445
 Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
 450 455 460
 Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Lys
 465 470 475 480
 Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser
 485 490 495
 Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
 500 505 510
 Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
 515 520 525
 Asn Leu Thr Ile Thr Ser Arg Phe Gln Glu Tyr Leu Asn Asp Leu
 530 535 540
 Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
 545 550 555 560
 Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Glu
 565 570 575
 Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
 580 585 590

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
 595 600 605
 Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys
 610 615 620
 Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp
 625 630 635 640
 Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
 645 650 655
 Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
 660 665 670
 Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
 675 680 685
 Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln
 690 695 700
 Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
 705 710 715 720
 Asp Leu Gln Gln Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
 725 730 735
 Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
 740 745 750
 Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
 755 760 765
 Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
 770 775 780
 Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
 785 790 795 800
 Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
 805 810 815
 Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
 820 825 830
 Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
 835 840 845
 Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala
 850 855 860
 Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
 865 870 875 880
 Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe
 885 890 895
 Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
 900 905 910
 Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
 915 920 925
 Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
 930 935 940
 Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
 945 950 955 960
 Lys Cys Phe Leu Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
 965 970 975
 Ser Asp Thr Cys His Ser Tyr Gly Gln Thr Leu Pro Ser Val Leu Ser
 980 985 990
 Gln Ile Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
 995 1000 1005
 Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn Lys
 1010 1015 1020
 Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro Leu Leu
 1025 1030 1035 1040
 Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu Glu Ser
 1045 1050 1055
 Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys Ser Pro Phe Thr
 1060 1065 1070
 Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg His Phe Val Ser Leu
 1075 1080 1085
 Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg Gln Thr Leu Gln Asn Ala
 1090 1095 1100
 Ser Glu Thr Val Lys Tyr Leu Asn Asn Leu Tyr Lys Ile Ile Pro Lys
 1105 1110 1115 1120
 Thr Leu Thr Trp His Ser Ala Lys Arg Glu Cys Leu Lys Ser Asn Met
 1125 1130 1135
 Gln Leu Val Ser Ile Thr Asp Pro Tyr Gln Gln Ala Phe Leu Ser Val

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 1140 1145 1150
 Gln Ala Leu Leu His Asn Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln
 1155 1160 1165
 Asp Asp Glu Leu Asn Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe
 1170 1175 1180
 ser Arg Trp Ala Glu Thr Asn Gly Gln Leu Glu Asp Cys Val val Leu
 1185 1190 1195 1200
 Asp Thr Asp Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro
 1205 1210 1215
 Gly Ala Ile Cys Tyr Tyr Ser Gly Asn Gln Thr Glu Lys Glu Val Lys
 1220 1225 1230
 Pro Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp
 1235 1240 1245
 Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Thr Lys Asn Arg
 1250 1255 1260
 His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln Lys Leu
 1265 1270 1275 1280
 Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys Glu Asn Asn
 1285 1290 1295
 Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met Ala Ser Trp Val
 1300 1305 1310
 Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu Met Trp Phe Asp Lys
 1315 1320 1325
 Thr Pro Leu Ser Tyr Thr His Trp Arg Ala Gly Arg Pro Thr Ile Lys
 1330 1335 1340
 Asn Glu Lys Phe Leu Ala Gly Leu Ser Thr Asp Gly Phe Trp Asp Ile
 1345 1350 1355 1360
 Gln Thr Phe Lys Val Ile Glu Glu Ala val Tyr Phe His Gln His Ser
 1365 1370 1375
 Ile Leu Ala Cys Lys Ile Glu Met Val Asp Tyr Lys Glu Glu His Asn
 1380 1385 1390
 Thr Thr Leu Pro Gln Phe Met Pro Tyr Glu Asp Gly Ile Tyr Ser val
 1395 1400 1405
 Ile Gln Lys Lys Val Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln
 1410 1415 1420
 Ser Gly Gly His Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe
 1425 1430 1435 1440
 Leu Glu Asp Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu
 1445 1450 1455
 Ser Ser His Asp Gly Ser Glu Ser Ser Ser Phe Glu Trp Ser Asp Gly Ser
 1460 1465 1470
 Thr Phe Asp Tyr Ile Pro Trp Lys Gly Gly Thr Ser Pro Gly Asn Cys
 1475 1480 1485
 Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His glu Lys Cys Asn Ser
 1490 1495 1500
 Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Ser Lys Ser Lys Leu
 1505 1510 1515 1520
 Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys Glu Asn Gly
 1525 1530 1535
 Ser Arg Trp Ile Gln Tyr Lys Gly His Cys Tyr Lys Ser Asp Gln Ala
 1540 1545 1550
 Leu His Ser Phe Ser Glu Ala Lys Lys Leu Cys Ser Lys His Asp His
 1555 1560 1565
 Ser Ala Thr Ile Val Ser Ile Lys Asp Glu Asp Glu Asn Lys Phe Val
 1570 1575 1580
 Ser Arg Leu Met Arg Glu Asn Asn Asn Ile Thr Met Arg Val Trp Leu
 1585 1590 1595 1600
 Gly Leu Ser Gln His Ser Val Asp Gln Ser Trp Ser Trp Leu Asp Gly
 1605 1610 1615
 Ser Glu Val Thr Phe Val Lys Trp Glu Asn Lys Ser Lys Ser Gly Val
 1620 1625 1630
 Gly Arg Cys Ser Met Leu Ile Ala Ser Asn Glu Thr Trp Lys Lys Val
 1635 1640 1645
 Glu Cys Glu His Gly Phe Gly Arg Val Val Cys Lys Val Pro Leu Gly
 1650 1655 1660
 Pro Asp Tyr Thr Ala Ile Ala Ile Ile Val Ala Thr Leu Ser Ile Leu
 1665 1670 1675 1680
 Val Leu Met Gly Gly Leu Ile Trp Phe Leu Phe Gln Arg His Arg Leu
 1685 1690 1695

DOI: 10.1007/s00339-007-0301-2

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List.Text 07.24.03.txt
His Leu Ala Gly Phe Ser Ser Val Arg Tyr Ala Gln Gly Val Asn Glu
1700 1705 1710
Asp Glu Ile Met Leu Pro Ser Phe His Asp
1715 1720

<210> 146
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker.

<400> 146
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 147
<211> 1518
<212> DNA
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

<210> 148
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

```

<400> 148
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
      1           5           10          15
Val Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ser
      20          25          30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Glu Gln Lys Pro Gly Ser ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys
260 265 270
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495
Pro Gly Lys

<210> 149

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

210 150

~~210~~ 150
~~211~~ 482

~~212~~ 182
212 PBT

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 150

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
260 265 270
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
275 280 285
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
290 295 300
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
305 310 315 320
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
325 330 335
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
340 345 350
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
355 360 365
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
370 375 380
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
385 390 395 400
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
405 410 415
Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
420 425 430
Ser Ser Ala Lys Pro Cys Gly Gln Ser Ile His Leu Gly Gly Val
435 440 445
Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
450 455 460
Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
465 470 475 480
Leu Glu

<210> 151

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 151

aagcttgcg ccattggatt tcaagtgcg attttcagct tccgtcaat cagtgccttc 60
gtcataattt ccaggaggaca aatttgttcc tcccgatctc Cagaacatct gtcgcacatct 120
ccaggggaga aggtcacaaat gactgtcagg gccagctcaa gtgtaaatgtt catgcactgg 180
taccaggcaga agccaggata ctccccaaa ccttgattt atgcccate caacccgtgg 240
tcttggatct ctgtctgcctt ctagtggcagt ggttctggaa cccttaactc ttccacaat 300
agcagaggatc aggttcgaaga tgctgcacat tattactggc agcagtggag tttaaaccc 360
cccacgttcg gtgtctggggac caagtggag tgaaaggatg gggtgtggctc ggccgtgtgt 420
ggatctggaa gaggtggggat cttcgcggat taatcacagc agtctggggc tqaqctgggt 480
aggcttgggg cctctggatc gatgtcctcg aaggcttcg gtacacatcatt tacaggatc 540
aatatgtcact gggtaaaagca gacccatcg aaggccctgg aatggatgg agcttatttat 600
ccggaaatgt gtgtatcttc ctacaatcg aagttaaagg gcaaggccac actgactgtt 660
gacaaaatccct ccacgcacatc ctacatcg gacatcgcc tgacatctgtg agactctcg 720
gtcttatttc gtgtcaaggat ggtgtactat agtaacttctt actgtactt cgtatgtctgg 780
ggcacaggga ccacgggtcac ctgtctccat ccagaaaaaca gctttaaat gcaaaaagggt 840
gatcagaatc ctcaaaatgc ggccatcgatc ataatgtggg ccacgcgtaa aacaacatct 900
gtgttacatc gggtctggaaat aggatactac accatggagca acaacttggg aaccttggaa 960
aatggggaaaat agctgaccgt taaaagacaa ghaacttcatat atatctatgc ccaagtcc 1020
ttctgttcca atccggaaagc ttcgatgtcaaa gctccatattt tagccaggct ctgccttaaag 1080
tccccccgtt gattcgagag aatcttactc agacgtcgaa atacccacag ttccggccaaat 1140
ccttgcgggc aacaafccat tcataatgggaa ggatgtttt aatgtcaacc aggtgtctcg 1200
gtgtttgtca atgtgactga tccaaaggcaaa gtgagccatc gactggctt cagctgtctt 1260
ggcttactca aactcgatgt ataatctgaa 1290

<210> 152

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> Mouse-Human hybrid fusion protein

<400> 152
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 305 310 315 320
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 325 330 335
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 340 345 350 355
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 365
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 370 375 380
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 385 390 395 400
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 405 410 415
 Gly Leu Leu Lys Leu Glu
 420

<210> 153

<211> 3630

<212> DNA

<213> Homo sapiens

<400> 153

atacgggaga actaaggctg aaacctcgga ggaacaacca cttttaagt gacttcgcgg 60
 ctgtgcgttttg gtgcgacta ggtggccccc ggccccgtgt gctggagccct gaagtccacg 120
 cgcgcggctg agaacccggc ggaccgcacg tggccgcggc gcgcitcccc cgcttccccag 180
 gtggggccggc gccgcggcggc cacctcaactg ccggccccgg gatgcgcgt ccccttcggc 240

<210> 154
<211> 595
<212> PRT
<213> *Homo sapiens*

<400> 154
 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
 1 5 10 15
 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
 20 25 30
 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
35 40 45
Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
50 55 60
Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65 70 75 80
Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr
85 90 95
Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
100 105 110
Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
115 120 125
Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln
130 135 140
Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
145 150 155 160
Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
165 170 175
Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met
180 185 190
Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu
195 200 205
Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp
210 215 220
Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Gly Ser Gly Asp Cys
225 230 235 240
Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
245 250 255
Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro
260 265 270
Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
275 280 285
Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
290 295 300
Ile Cys Ala Ala Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
305 310 315 320
Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
325 330 335
Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
340 345 350
Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
355 360 365
Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
370 375 380
Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly
385 390 395 400
Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
405 410 415
Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
420 425 430
Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
435 440 445
Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Arg Gly Leu Met
450 455 460
Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
465 470 475 480
Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Pro Ser Ser
485 490 495
Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
500 505 510
Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
515 520 525
Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
530 535 540
Glu Pro Glu Leu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
545 550 555 560
Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
565 570 575
Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
580 585 590

2011-01-01

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Ser Gly Lys
595

<210> 155
<211> 1824
<212> DNA
<213> *Homo sapiens*

<210> 156
<211> 547
<212> PRT
<213> *Homo sapiens*

```

<400> 156
Met Ala Thr Met Val Pro Ser Val Leu Trp Pro Arg Ala Cys Trp Thr
      1          5          10          15
Leu Leu Val Cys Cys Leu Leu Thr Pro Gly Val Gln Gly Gln Glu Phe
      20         25          30
Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser Ala Gly Gly Ser
      35         40          45
Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser Glu Lys Ile Ala
      50         55          60
Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser Gly Met Gly Trp
      65         70          75          80
Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg Ile Leu Cys
      85         90          95
Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser Asn Ile Thr
      100        105          110
Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Pro Trp
      115        120          125
Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val Glu Gly Gly
      130        135          140
Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp Glu Glu Glu
      145        150          155          160
Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu Val Thr Ala Glu

```


49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

ttttttgtagt	tttagtagag	acggaatttc	gccatgttag	ccagactgt	cttgcacttc	780
ttgacctcagg	tgatccaccc	gccttggct	cccaaagtgc	tgggattaca	ggccggggcc	840
accgtgcctc	qccatgggt	tctgtctcac	catggctgig	gtcactgtg	cicagactgt	900
gtcttggcca	tacaaggggg	accatgtttc	agcagtgcac	cagccccgaa	gttgcacact	960
gaggagttgc	ctctccigac	tcagtgcgc	ctcagtttac	ccacgtgtc	catggaccc	1020
tttgtcgagg	gtcgaacccgc	aggccaggcc	ctactgtgc	ctggggctcg	aacacgggtt	1080
tcttgggca	aaggggtcag	aaggcagaat	aaggccatgc	ttgggggtgc	cagaccccgc	1140
Ctttgtgc	agccccacage	cagggtcccc	ggccgtccac	cttccttc	ccgcctccgc	1200
tgcccccttc	ccctctcc	cccccttc	cacagtcctt	ataggccacat	ccccgaaagg	1260
aaacccagac	tctggcgcac	gcagagacga	ggatgtcg	gggggtctgg	cggtctgggg	1320
ggcggtgt	tcgcgtctg	cttcctctgg	ggcttgggtc	gagcacccgt	agggggttc	1380
actgtgtcg	ggacacccat	ccccagaa	accgtgtc	cicagactgt	aggccagggt	1440
aggccctcagg	agggggtcgc	acgcacgggc	actccaggaa	ttgggggtcg	ggggccggat	1500
ggggcagcc	ggaggctgtgt	cttgggggg	gggggggtga	ggggccggcc	aacgtgttgc	1560
gaggagccgc	tttttttttt	ccacggggcc	aaaggctggg	cttgcaccc	tttttttttt	1620
ggccctgtgt	cgaggcaca	ggatgtgt	cgctgtc	cgicccccaa	acacgtgtgt	1680
Ccgatcg	ggggccggcc	tctacaacga	ctgtgtc	tccaaagggt	gaaaggccgt	1740
cacgtgtgtt	aaacctgtgt	agtcgtccac	ggggccccc	ggcccccaca	gacagggggg	1800
cgccagccgt	gcacccat	tccacacac	caacatggg	ctccacacgc	cgccagaaaa	1860
aacctcaaa	cacacgggg	tctgtccgc	caacagggtc	tttttttttt	tttttttttt	1920
cttccagggg	caccccttc	ccccccgggg	ggcccaaaact	ggcccaaggcc	acgtgtgttc	1980
ggggagacca	cgtgtccat	gttggccgt	cttgcgtgg	ttgggggtgg	gggggggggg	2040
ttggggcat	gagacccatgc	cgacgggg	tttttttttt	gggggggtgg	gggggggtgg	2100
gaagggtgt	tttttttttt	acggaaaccc	ccccccgtgt	tttttttttt	tttttttttt	2160
aggaggctcg	ggggccgtcg	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2220
ggccgttgt	tttttttttt	ggggcccaaa	tttttttttt	tttttttttt	tttttttttt	2280
tgccacacag	ccccccatcg	ccccccatcg	tttttttttt	tttttttttt	tttttttttt	2340
cgccggaa	ctgtgtcg	ccccacacgg	tttttttttt	tttttttttt	tttttttttt	2400
gccccctgg	agactaacac	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2460
gggtgtcgat	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2520
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2580
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2640
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2700
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2760
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2820
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2880
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2940
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3000
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3060
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3120
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3180
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3240
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3300
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3360
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3420
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3480
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3540
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3600
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3660
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3720
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3780
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3840
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3900
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3960
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4020
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4080
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4140
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4200
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4260
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4320
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4380
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4440
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4500
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4560
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4620
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4680
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4740
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4800
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4860

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

tgaatgaaa	tgaccacagc	gacttcatgt	aacgtggccc	Cacagtggag	aaacccaggc	4920
atccgc	cagc	agcgtggatg	cgcgactgt	ggcgatgtca	gatgagctcc	4980
gccccaccca	cagggttcca	cagacgttcc	caaggccctg	gggcggctcc	cgccggctcg	5040
ggaatctttc	caagctgttg	tctggagtg	gggtatccct	cgagcagcac	agagcctgct	5100
cccgagcggc	agtccacaccc	gagaccacag	ctcgggaaaca	agacgggagc		5150

<210> 158
<211> 277
<212> PRT
<213> Homo sapiens

<400> 158

Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Cys	Ala	Ala	Leu
1				5				10						15	
Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val
				20				25					30		
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro
	35					40						45			
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys
	50					55						60			
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro
	65					70				75				80	
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys
						85			90				95		
Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	cys	Arg	Cys	Arg	Ala	Gly
	100					105							110		
Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys
	115					120							125		
Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp
	130					135						140			
Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn
	145					150				155				160	
Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro	Ala	Thr	Gln	Pro
						165				170				175	
Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr	Val	Gln	Pro	Thr
	180					185							190		
Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr	Arg	Pro	val	Glu
	195					200							205		
Val	Pro	Gly	Gly	Arg	Ala	Val	Ala	Ala	Ile	Leu	Gly	Leu	Gly	Leu	Val
	210					215						220			
Leu	Gly	Leu	Leu	Gly	Pro	Leu	Ala	Ile	Leu	Leu	Ala	Leu	Tyr	Leu	Leu
	225					230						235			240
Arg	Arg	Asp	Gln	Arg	Leu	Pro	Pro	Asp	Ala	His	Lys	Pro	Pro	Gly	Gly
						245					250			255	
Gly	Ser	Phe	Arg	Thr	Pro	Ile	Gln	glu	Glu	Gln	Ala	Asp	Ala	His	Ser
	260					265							270		
Thr	Leu	Ala	Lys	Ile											

<210> 159
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 159

ccacgcgtcc	gagaccaagg	agtggaaagt	tctccggac	ccctggatc	tcaagagtga	60
catttgtgac	accgactta	ttgataaaa	ttcttcttgg	atcagctttg	ctttagtatcat	
acgttgtcgc	gatttcata	tggaaacag	ctgttacaa	atagtagcca	ctctgttgtc	180
ggctcttcac	tttgagaggaa	caagatcatt	gcaggatctt	tgtatgtact	gccccagcttg	240
tatatttcgtt	gataataaca	ggaatcatt	tttgcgttcc	tgtccctccaa	atatgttctc	300
caggcgttgt	ggacaaaagg	cttgcgtatc	atgcggac	tgtaaaagggt	ttttcaggac	360
caggaaaggag	ttttcccca	ccaccaatgc	aggatgtgc	tgcacttcag	ggtttcactg	420
cctggggggcc	ggatgcggca	tgtgttgcac	ggatgttcaa	caaggtcaag	aactgttacaa	480
aaaatgttgtt	aaagactgtt	gtttggggac	atttaacgt	cagaaacgtg	gcactgttgc	540
accctggggca	aactgttctt	tgtatggaaa	gtctgttgc	gtgttaatggaa	cgaaaggagag	600
ggacgttgttgc	tgttgacat	tttcggccca	cccttcctcc	ggagcatcc	cttgtgacc	660

WO 2005/037989

PCT/US2003/024918

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gcctggccct gcgagagac caggacactc tcccgacatc atcttccttct ttcttcgcct 720
gacgtgcact gctgttgctc ttctgtgtt ctccctcaq ctccgtttcc ctgttgtaa 780
acggggcaga aagaactcc tgatataattt caaacacca tttatgagac cagtacaaa 840
tactcaagag gaagatggct gtatgtccg atttccagaa gaagaagaag gaggatgtga 900
actgtgaaaat ggaatcaat agggtgttg ggacttctt gaaaagaagc aaggaaatat 960
gagtcatccg ttatcacage tticaaaaagc aagaacacca tcctacataa taccaggat 1020
tcccccaaca cacgtttctt ttctaatgccc aatgagtggg ctttttaaaaa tgacccactt 1080
ttttttttttt ttggacagg gtctcaatct gtccacccgg ctggagggtca gtggcaccac 1140
catggcttc tgcacccctg acctctgggg aactcaaggta tccctctggcc tcaatgttctt 1200
gagtagctgg aactacaagg aaggccacc acacttgact aactttttg ttttttttttg 1260
gtaaagatgg catttcggca tggtgtatcg gctggctca aactctctagg ttcaactttgg 1320
ccttcggaaag tgctgggattt acagacatga tgcctccaggc cggccaaaaa taatgcacca 1380
cttttaacag aacagacaga tgaggacaga gctggat 1419

```

<210> 160

<211> 255

<212> PRT

<213> Homo sapiens

<400> 160

```

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1 5 10 15
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
20 25 30
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
35 40 45
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
50 55 60
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65 70 75 80
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
85 90 95
Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110
Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125
Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys ser Leu Asp Gly Lys
130 135 140
Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145 150 155 160
Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
165 170 175
Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
180 185 190
Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
195 200 205
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
210 215 220
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240
Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

```

<210> 161

<211> 5784

<212> DNA

<213> Homo sapiens

<400> 161

```

aaaataataat tattaggca acattataaa atgtcaatcc ttgtttttt tctttttttt 60
tatcgaggaa aaatcaatgg ttctggcaat ttatgtatgtt ttatatttca caacggagggt 120
gtacaaattt tatgtcaataa ttctgcacatt gtcccgacat tttaaatgtca gtgtcgaaaa 180
ggggggcaga tacttcgtca ttctcataag acaaaaaggaa gtggaaaacac agtggtcatt 240
aaggtctga aatttcgtca ttctcgatgtt tccaaacaca gtgtcttttt ttcttataatc 300
aacttggacc atttcgtatgc caacttatac ttctgcaccc ttcaatattt tgatctccct 360
ccttttaaag ttaactttac agggaggat ttgtatgtt atggtaagac atgtcttca 420
tcttcaccaac ttaaagatgtt tgacaaactt tctcaactt aaaaatcaattt 480
agacaaataaa atatcttttg ttgtggatgtt cacttagat cagttgtatgg taatcaat 540

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

taatgaagat	atacagggtga	tgatttacta	ttaatcataa	tttagtattat	tcaagaaat	600
gcatgtat	cccatagact	gctaagtcat	aaatagatca	tatigccctt	taaacatata	660
tgcttataaa	aatcgaaa	aacattaaga	caaactacta	aacttatggc	ttaaatggat	720
gttattatctc	tattcaccta	agatttaaag	tttggttttg	cactgtgtt	gttggaaatgg	780
tgatgatgat	tgaaaaatcat	agttttataa	cattacttt	actattact	cttttataaa	840
aataataggca	gaaaagccct	ttcttataaa	cacatttgc	aatacattat	atgcataatc	900
ttttaaatgg	tagttccctgg	atccttgca	taaacttg	atgtatgg	tcaataact	960
tgcacactt	ttggatittc	tgactataat	aaagaaaaagc	ttccatgtat	taaatagtc	1020
tttttaaattt	ggtlaagagaa	cttgcgttgc	agcagaattt	ttccatataa	tcacctttt	1080
tccaaatccg	aatccaaact	tttgtccgg	ttcaatgttc	gttaccat	aggatgtgc	1140
gccttttgtt	tagttgtcg	ttttggatgc	atattttat	tttgcgttca	tttttttttt	1200
aggcattttc	atctttcttc	gtatctgtc	catagatgc	catcgtgtat	tattttcttc	1260
tcaaaatgg	acatgcgttc	tgtagagata	atttggacaa	caggggatcc	atcccttc	1320
ccccaaagat	actactaaat	taaactatac	acttggaa	gaaattttat	tattttttt	1380
atagccccc	cattttcaag	aggacttgc	ttatgtatc	acagagatgt	atcattttat	1440
tatttttgtt	caaaactat	gaggaaattt	ttgtatgc	tttttttttt	tttttttttt	1500
aggttttaaaat	atcaaaatgt	atgtatgtca	tttttttttt	tttttttttt	tttttttttt	1560
aattttgtatc	caagggttcc	gaggaggcgg	gcagagatgc	tttttttttt	tttttttttt	1620
gttttttgtt	taaigttttt	acagtcgcg	aaagaaatcc	tttttttttt	tttttttttt	1680
gagaaggaaa	tttgcacactt	ttttttatgt	tttttttttt	tttttttttt	tttttttttt	1740
aaccactgt	gaggtttttt	gaaatgtaaa	tttttttttt	tttttttttt	tttttttttt	1800
gtttttggat	attttttttt	gtctcttgca	ttacatgttc	tttttttttt	tttttttttt	1860
actttttttt	ttacatgttc	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1920
atgtttttat	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	1980
tagccccc	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2040
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2100
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2160
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2220
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2280
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2340
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2400
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2460
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2520
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2580
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2640
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2700
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2760
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2820
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2880
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	2940
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3000
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3060
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3120
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3180
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3240
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3300
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3360
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3420
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3480
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3540
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3600
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3660
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3720
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3780
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3840
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3900
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	3960
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4020
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4080
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4140
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4200
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4260
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4320
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4380
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4440
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4500
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4560
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4620
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	4680

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

caacagccac ttcataataga gagctatgtc ttacattctt tcctctgtg ctaaatgtt 4740
ttatataatc atgcatacat atatacacac atgtatgtt aaaatttcata atgaatataaf 4800
ttgcttarat ttcctccata agaaatattt tgctccagaa agacatgtc ttttcttaaa 4860
ttcaggtaaa atggtttact tggtaaagt tagtgttagg aaacatgtcc cggaaatggaa 4920
agcaaattt ttttatttata ctatttcta ccattatcta tggtttcatg gtgtctatfaa 4980
ttacaagttt agttctttt gtatgtatc taaaattgc aaacaaaatc atcttttaatg 5040
ggccagcatt ttcatgggggt agagcagaat attcatttag ctgtaaagct gacggttacta 5100
taggttgtcg tcaagactata ccacatgtc ctctgggtt gacaggtcaaaatgttcccc 5160
atcaggcttg agcagcccccc caagaccgtt gggaaatccc ggttgtggag actccccctga 5220
gccagggcc acttaggtttt ctgttccca gaggtgttca gacccctggg aatccacagt 5280
gttacccatcg attcataattt ccaggatctg tgaaagcacat gggcacaaat 5340
cccttcataaaa acacacac agcctggaa ttggccctgg cccttcataa tagcccttt 5400
tagaaatattt ttgtgttaga aaatgttca aatatgttggaa atatgtttagt ttcgtgtt 5460
aatattttt ctacttcctg ttcgtatgcc caaaggcttc gaagcagccaa atgtcgtatg 5520
aacaacattt gtaactttaatg gtaaaatgtgg attatgttgg attttaacat ttgttactg 5580
tgtgtttata ttgttcaatg gaaacccgtt gtaactttaatg gtaactttaatg 5640
gcatgtgtt gtcgtgtatg gtacagatca gtaactttaatg gtaaatttga atctgtatg 5700
tgtrifctgtt ttcaactgtt gttggacaacc tgactggctt tgacagggtg ttccctgtgt 5760
tgtttgcagg ttctgtgtgt tgggg
```

<210> 162
<211> 199
<212> PRT
<213> Homo sapiens

<400> 162

Met	Lys	Ser	Gly	Leu	Trp	Tyr	Phe	Phe	Leu	Phe	Cys	Leu	Arg	Ile	Lys
1				5					10				15		
Val	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asn	Tyr	Glu	Met	Phe	Ile
	20				25				25			30			
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Leu	Cys	Lys	Tyr	Pro	Asp	Ile	Val
	35				40				40			45			
Gln	Gln	Phe	Lys	Met	Gln	Leu	Leu	Lys	Gly	Gly	Gln	Ile	Leu	Cys	Asp
	50				55				55			60			
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Thr	Val	Ser	Ile	Lys	Ser	Leu
	65				70				70			75			80
Lys	Phe	Cys	His	Ser	Gln	Leu	Ser	Asn	Ser	Asn	Ser	Val	Ser	Phe	phe
	85				85				85			90			95
Tyr	Asn	Leu	Asp	His	Ser	His	Ala	Asn	Tyr	Tyr	Phe	Cys	Asn	Leu	Ser
	100				100				105			105			110
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Lys	Val	Thr	Leu	Thr	Gly	Gly	Tyr	Leu
	115				115				120			120			125
His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Phe	Trp	Leu	Pro
	130				130				135			140			
Ile	Gly	Cys	Ala	Ala	Ala	Phe	Val	Val	Val	Cys	Ile	Leu			
	145				145				150			155			160
Ile	Cys	Trp	Leu	Thr	Lys	Lys	Tyr	Ser	Ser	Ser	Val	His	Asp	Pro	
	165				165				170			170			175
Asn	Gly	Glu	Tyr	Met	Phe	Met	Arg	Ala	Val	Asn	Thr	Ala	Lys	Lys	Ser
	180				180				185			185			190
Arg	Leu	Thr	Asp	Val	Thr	Leu									
	195														

<210> 163
<211> 822
<212> DNA
<213> Homo sapiens

<400> 163

gggtctgtcc	acgtttttgc	cggagacaga	gactgtatcg	gaaacagggga	aggggctggc	60
tgttcctcatc	ctgttctatca	ttcttcttca	aggttacttg	gccccagtc	tccaaaggaaaa	120
ccacttgtt	aagggtatg	actatcaaga	agatgttgc	gtacttctgt	cttgcgtgc	180
agaagccaaa	aatatcataat	gtttttaaa	tggggatgt	atccggcttc	taactgttgc	240
aaaaaaaaaa	tggaaatctgg	gaagatgtatc	caaggacacct	cgagggtatgt	atctgtatgt	300
aggatcacag	acaatgttcc	aaccacttca	atgttattac	agaatgtgtc	agaatgtatgt	360
tgaacttaat	gcagccacca	tatctggctt	tctttttgtt	gaaaatgtca	gcattttcggt	420

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 cttctgtt gggctact tcattgtgg acaggatggaa gtcgcaggat cgagac 480
 agacaacgca actctgttc ccaatgtccac gcttcacccat cccctcaagg atcgagaaga 540
 tgaccatgtt acccacccatc aaggaaacca gttggaggaa aatgttcaactt agggacttca 600
 gtatgtccagg tggttccctt ctatccgtt cccagaatca aagcaatgtca ttgtggaaag 660
 ctcttagcag agagacttcc agccccatatt ctgacttcaa gtttcccaaa gatgacaata 720
 ggagaagaaa ggccatcaga gcaaatttgg ggtttctca aataaaaataa aaataaaaac 780
 aataactgtt ttccatcaga gcccacccat gggggaaaattt gt 822

<210> 164

<211> 182

<212> PRT

<213> Homo sapiens

<400> 164

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
 1 5 10 15
 Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys
 20 25 30
 Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
 35 40 45
 Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe
 50 55 60
 Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
 65 70 75 80
 Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
 85 90 95
 Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
 100 105 110
 Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
 115 120 125
 Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
 130 135 140
 Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
 145 150 155 160
 Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
 165 170 175
 Asn Gln Leu Arg Arg Asn
 180

<210> 165

<211> 1311

<212> DNA

<213> Homo sapiens

<400> 165

gtaaatctcg tggccctccg catcttagta aagtaacagt cccatgaaac aaagatgcag 60
 tcggccactc actyggagat tctggccctc tgcccttat cagttggcg tggggggcaa 120
 gatggtaatg aagaatgggg tggttattaca cagacccatc ataaatgttc catctctgg 180
 accacatgtt attggatcatc cccctcgtat cctggatctg aaataactatg gcaacacaaat 240
 gataaaaaatc taggcgttgat tgaggatgtt aaaaatcatatg gcaatgttgaa ggttccatctg 300
 tcacttgaaatg aatitccatc atttggacaa atgggtttat atgttcgttca ccccgaggaa 360
 agcaacacccaa aagatgcgaa cttttatctc taccctggggg caaagatgttg tgaaactgc 420
 atggagatgg atgtgtatgc ggtggccaca attgttcatatc tggaatctcg catcactgg 480
 ggcttgcgtcg tgctgggttta ctactggacg aagaatagaa aggccaaaggc ctagccctgtg 540
 acacggggatc cgggttctgg cggcaggccaa aggggacaaa acaaggagag gcccacccat 600
 gttcccaaccat cagaatgttgc gccatccgg aaaggccatc ggacatctgat ttctggccctg 660
 aatcggatgcg gcattctggacc ctctggagaaa cactgcctcc cgctggccca ggttccctct 720
 ccagtccccc tggcactcccc ttgttccctgg gctgttctt gaccatccatc gagagaaatcg 780
 ttccatccatc tcatgttgaaat ctggccctt ccacgttcatatc ccccgcttcc ttctccctgt 840
 ctccatctgtt tggttccatccg tctttaaaaat ttgttcttcc ttctccctttt gaatgtatcat 900
 ctagatgttcc acccttcacatc ttggccctgg ctttgcctat gatattttttt tggttcttcc 960
 atcccttcctt cttttgtatgc aacttctcg ttcatgttcc ttctttttttt tggttcttcc 1020
 tgccccccat cccaaatgtt cccatctact ttcttctatcg ctgtcccttt tgacggccctc 1080
 tctggggatgc gactggatgtt atgttgcacg aggccctgtcc cctgttccatc atttttggcc 1140
 tgagccatgc ctgttctcc ctccatccccca acacttccatc ccaacccctt atcccttcat 1200
 tccctccaaat cccccccccc atctgttgcacg atctgtatgtt cattttggcat ctccgttatat 1260
 gtgtctctgg tcctcagatc agagagaaaa aaataaaatgtt tattttggctg c 1311

WO 2005/037989

PCT/US2003/024918

<400> 49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 166

<211> 207

<212> PRT

<213> Homo sapiens

<400> 166

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
 1 5 10 15
 Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
 20 25 30
 Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
 35 40 45
 Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
 50 55 60
 Asn Ile Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
 65 70 75 80
 His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
 85 90 95
 Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
 100 105 110
 Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
 115 120 125
 Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
 130 135 140
 Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
 145 150 155 160
 Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
 165 170 175
 Lys Glu Arg Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
 180 185 190
 Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
 195 200 205

<210> 167

<211> 3

<212> DNA

<213> Homo sapiens - to be filled in

<220>

<221> misc_feature

<222> 1, 2, 3

<223> n = A,T,C or G

<400> 167

nnn

3

<210> 168

<211> 2

<212> PRT

<213> Homo sapiens - to be filled in

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 168

Xaa Xaa

1

<210> 169

<211> 3084

<212> DNA

<213> Homo sapiens

<400> 169

ctgggctccgttgcagag ctccaagtcc tcacacatgc acgcctgttt gagaaggcgc 60

WO 2005/037989

PCT/US2003/024918

49O76.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 85 90 95
 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
 100 105 110
 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
 115 120 125
 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
 130 135 140
 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
 145 150 155 160
 Lys Asn Ile Gln Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
 165 170 175
 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
 180 185 190
 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
 195 200 205
 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
 210 215 220
 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
 225 230 235 240
 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
 245 250 255
 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
 260 265 270
 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
 275 280 285
 Pro Gln Tyr Ala Gly ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
 290 295 300
 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
 305 310 315 320
 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr ser Pro
 325 330 335
 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 340 345 350
 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 355 360 365
 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
 370 375 380
 Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile
 385 390 395 400
 Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile
 405 410 415
 Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met
 420 425 430
 Ser Gln Ile Lys Arg Leu Leu Ser Glu Lys Lys Thr Cys Gln Cys Pro
 435 440 445
 His Arg Phe Gln Lys Thr Cys Ser Pro Ile
 450 455

<210> 171
<211> 2308
<212> DNA
<213> Homo sapiens

<400> 171
 gaaatcgacttg atggaccac aagggtgaca gcccaggcg accgatcttc ccattccaca 60
 tccctccggcg cgatggccaa aagaggctga ggcaactgg gccttctgc gaaaaagacc 120
 tccgcgtcac tgccccggct gggtccaaagg gtggatcata cctgtgtat 180
 tggggactgc tcacgttcat catggtgcct ggtgcggag cagagctctg tgacgtatg 240
 cggccagaga tc cccacatgc caccatcaat gccatgtttt acaaaaggcg ggtaactcta tatgttctgt 300
 aacttgtaat gcaagagagg ttccgcaga ataaaaaggcg aatgcacaatg ctgcggact 360
 acaggaaact ctggccacte gtccggatc gaccaatgtc aatgcacaatg ctgcggact 420
 cggaaaccaa gcaaaaactg gacaccatc ctggaaagac agaaaagaaac gaaaaccaca 480
 gaaatcgaaa gtcccaatgtca gtcggatggc caagcgagcc ttccggatca ctgcggagaa 540
 cttccaccat ggaaaaatgtc accgcacagg agaaatttgc atttgcgtgtt gggcagatgt 600
 gtttattatc atgtcgctca ggatggatcagg gcttacatca gagggttccgtc tgaaagcg 660
 tgcaaatgtg cccacggggaa gacaagggttgg accccaggcccc agcttataatg cacagggttgg 720
 atggagacca gtcagtttc aggtgttggag acggcttcagg caagccccga agggccgtct 780
 gagagtgaga ctccctgcct cgtccacaac acagattttc aaatacagac agaaatggct 840

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

<210> 17

<211> 272

<212> PRT

<213> Homo sapiens

<400> 172

Met Asp Ser Tyr Leu Leu Met Trp Gly Leu Leu Thr Phe Ile Met Val
 1 5 10 15
 Pro Gly Cys Gln Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro
 20 25 30
 His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn
 35 40 45
 Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr
 50 55 60
 Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys
 65 70 75 80
 Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro
 85 90 95
 Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro
 100 105 110
 Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro
 115 120 125
 Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val
 130 135 140
 Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His
 145 150 155 160
 Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg
 165 170 175
 Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
 180 185 190
 Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu
 195 200 205
 Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
 210 215 220
 Met Ala Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
 225 230 235 240
 Val Ala Val Ala Gly Cys Val Phe Leu Leu Ile Ser Val Leu Leu Leu
 245 250 255
 Ser Gly Leu Thr Trp Gln Arg Arg Gln Arg Lys Ser Arg Arg Thr Ile
 260 265 270

<210> 173

WO 2005/037989

PCT/US2003/024918

<211> 1060 49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> DNA

<213> Homo sapiens

<400> 173

cggtccccc ggcgcctccc ctgcgcggc agcttcgagc caagcagcgct cctggggagc 60
 gcgtcatgc cttaaccatg accgccttgc tccgcggct ggccttgctg ctccacccgc 120
 ccaggcccg ccagttccgg tggtgcggc tggatccggac ctggaaacctg ggcgagacag 180
 tggagctgaa gtgcggatgt ctgtgttcca accgcacgc tcggctgtcg tggctttcc 240
 agccgcgcgg cgccgcgcgc agtccacact tcctccataa cctctcccaa aacaaagccca 300
 agccgcgcgg ggggtcgpac acccaacggt tctcgggcaa gaggttgggg gacacccctcg 360
 tccctaccct gagcgaactc cgccgagaga acggaggcta ctatttcgtc tcggccctcg 420
 gcaactccat catgtacatc agccacttc tgccgcgtc ctgcgcgcgg aagccaccga 480
 cgacgcgcggcc gcccgcgacc acaacaccgg cggccacccat cgccgtcgag cccctgtccc 540
 tgccgcggcaga ggccgtccgg ccagccgggg ggggcgcgat gacacacggg gggctgtggact 600
 tcgcctgtgtat tattttatc tggccgcct tggccggat ttgtggggtc ctttcttgc 660
 cacttgttat cacccttatac tggccgcct tggccggat ttgtggggtc aatgttcccc 720
 ggccgttgttccaaatcgggaa gacaaggccca gcaatccggc gagatcgtc taaccctgtg 780
 caacagccac tacattactt caaatcgaga tccctccctt tgaggaggaca agtccctccc 840
 tticattttt tcaggatctc ctccctgtgt attcatcttc atgattattt tttagtgggg 900
 ggcgggtgtgg aaagatgg tttttttttt tggtgttgac gggaaacaaa acttagttaaa 960
 atttttttttt caccacaaagg gtccacaatc tggccgcgc acatcgccgtt agggcgtggaa 1020
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1060

<211> 174

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
 20 25 30
 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gin Val Leu Leu Ser
 35 40 45
 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
 50 55 60
 Ala Ser Pro Thr Phe Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
 65 70 75 80
 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
 85 90 95
 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
 100 105 110
 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
 115 120 125
 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg
 130 135 140
 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 145 150 155 160
 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 165 170 175
 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
 180 185 190
 Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
 195 200 205
 Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
 210 215 220
 Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
 225 230 235

<211> 175

<212> DNA

<213> Homo sapiens

<400> 175

gaattccgtg gttcctcagt ggtgcctgca accccctgggtt caccctccctc caggttctgg 60

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

ctccttcag	ccatggctct	cagagtctt	ttgttaacag	ccttgaccct	atgtcatggg	120
tccaaacttgc	acactggaaa	cgaatgtacc	ttccaaggaa	acggcaagggg	cttcggggcc	180
agcgatgttc	aqcttcaggg	atccagggtt	ttggtttgag	cccccccaaga	gatatgttgt	240
gccaacccaa	ggggcagcct	ctaccaggc	gactacacga	cagggttcata	cgagccccatc	300
cgccgtcagg	ccccgttgg	ggccgtgaac	atgtcccttg	gcttgccttc	ggcagcccccc	360
accaggcccc	ttcagctgtc	ggccgttgtt	ccccaccgtgc	accagactgt	cagtggaaaa	420
acgtatgtta	aagggtctgt	cttccgtttt	ggatccaacc	tacggcagca	gcccagaag	480
ttcccaaggag	ccctccggagg	gtgtcttcaa	gaggatatgt	acatgtccct	cttgatgtat	540
ggcttggta	gcatcatccc	atgacttgc	cgccgtatgg	aggaggatgtt	ctcaatgttg	600
atggagcaat	taaaaaaagt	caaaaacctt	ttcttcatttg	tgcagtatct	tgaaaaattc	660
cggttttttt	ttatccatcc	agagttccat	tttttttttt	tttttttttt	actgtgttgg	720
ccaaataacgc	agctgttgg	cgggacacac	acggccacgg	gcatccggaa	atgtgttggaa	780
gagctgttta	atcatcacca	cgggggccga	aaagatgtcc	ttttagalgtt	atgtgttgcac	840
acgatggag	aaaaatgttg	cgatcccttg	ggatgtatgg	atgtcatcc	ttggggccgg	900
agagggagg	ttatccgtca	cgatgttttt	tttttttttt	tttttttttt	ttggggccgg	960
cgccaaagac	ttatataccat	cgatccaaag	cgccctcggt	atcagtggtt	ccagggtgtt	1020
aactttttgg	cttcgtaaag	cattccaaac	cgacttgggg	tttttttttt	ttggatgttgc	1080
gggttttttt	tttttttttt	cgatcccttt	ggatcatgg	tttttttttt	ttggatgttgc	1140
cggttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1200
ggggattttc	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1260
tcagatgtca	atgtatgttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1320
caaaaggcttgg	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1380
cagaacactg	gtatgtgggg	gttccaaatgt	atgttcgggg	tttttttttt	ttggatgttgc	1440
tttggggctt	cccttcgttc	cggtggatgt	ggacacacgg	tttttttttt	ttggatgttgc	1500
atcgggggcc	ccccatacta	cgagcagacc	cgagggggcc	tttttttttt	ttggatgttgc	1560
ccccgggggg	agggggtctg	gtggcgttgt	gttttttttt	tttttttttt	ttggatgttgc	1620
ccccgggggg	gttttttttt	ggcccttataa	tttttttttt	tttttttttt	ttggatgttgc	1680
acggacgttg	ccatggggcc	ccccgggggg	tttttttttt	tttttttttt	ttggatgttgc	1740
cacggggactt	ccaggatctgg	cattccggcc	tttttttttt	tttttttttt	ttggatgttgc	1800
cttcgttttttt	ggcccttggat	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1860
gtatgttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1920
ccatgttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	1980
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2040
catgtttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2100
ttatgttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2160
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2220
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2280
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2340
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2400
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2460
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2520
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2580
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2640
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2700
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2760
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2820
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2880
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	2940
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3000
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3120
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3180
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3240
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3300
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3360
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3420
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3480
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3540
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3600
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3660
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3720
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3780
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3840
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3900
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	3960
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	4020
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	4080
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	4140
tttttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	ttggatgttgc	4200

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
tgcccaactga ggaatcatga agcttccttt ctggattcat ttatatttc aatgtgactt 4260
taatttttt gatggataag cctgtctatg tgcacaaaat cacaaggcat tcagaatgtac 4320
agtggaaagt ctccttcc agatattcaa gtcacctcc taaaggtagt caagattgtc 4380
tttgtgggtt tcccttcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac 4440
accacacaca tacacacaca caacgtttt tacacaaaatg gtgatcatct ttatattgtt 4500
ctgtatcttg cttttttca ccaatatttc tcaagacatcg gtgtcatatgg agacataaaat 4560
tactttttca ttcttttata ccgctgcata gtatccattt gtgtgagigt accataatg 4620
attttaaccag tcttcttttg atatactatt ttcatctctt gtgtattgtc ctgctgagtt 4680
aaaaaatcaa atatatgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4740

<210> 176
<211> 1153
<212> PRT
<213> Homo sapiens

<400> 176
Met Ala Leu Arg Val Leu Leu Leu Thr Ala Leu Thr Leu Cys His Gly
1 5 10 15
Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
20 25 30
Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
35 40 45
Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
50 55 60
Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
65 70 75 80
Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
85 90 95
Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
100 105 110
Cys Ser Gln Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
115 120 125
Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
130 135 140
Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
145 150 155 160
Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
165 170 175
Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
180 185 190
Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
195 200 205
Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
210 215 220
Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
225 230 235 240
Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
245 250 255
Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
260 265 270
Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
275 280 285
Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
290 295 300
Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
305 310 315 320
Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
325 330 335
Gly Thr Gln Thr Gly Ser Ser Ser Phe Glu His Glu Met Ser Gln
340 345 350
Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
355 360 365
Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
370 375 380
Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
385 390 395 400
Asp Ala Tyr Leu Gly Tyr Ala Ala Ile Ile Leu Arg Asn Arg Val
405 410 415

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val
420 425 430
Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val
435 440 445
Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser val
450 455 460
Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
465 470 475 480
His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
485 490 495
Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
500 505 510
Glu Gln Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
515 520 525
Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
530 535 540
Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
545 550 555 560
Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
565 570 575
Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
580 585 590
Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
595 600 605
His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
610 615 620
Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
625 630 635 640
Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
645 650 655
His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
660 665 670
Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
675 680 685
Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
690 695 700
Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
705 710 715 720
Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
725 730 735
Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
740 745 750
Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
755 760 765
Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
770 775 780
Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
785 790 795 800
Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
805 810 815
Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
820 825 830
Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
835 840 845
Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
850 855 860
Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
865 870 875 880
Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
885 890 895
Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
900 905 910
Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
915 920 925
Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
930 935 940
Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
945 950 955 960
Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 965 970 975
 Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
 980 985 990
 Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
 995 1000 1005
 Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
 1010 1015 1020
 Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly Ile
 1025 1030 1035 1040
 Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe Asp Trp
 1045 1050 1055
 Tyr Ile Lys Thr Ser His Asn His Leu Ile Val Ser Thr Ala Glu
 1060 1065 1070
 Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro Gly Gln Gly Ala
 1075 1080 1085
 Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu Pro Phe Glu Val Pro
 1090 1095 1100
 Asn Pro Leu Pro Leu Ile Val Gly Ser Ser Val Gly Gly Leu Leu Leu
 1105 1110 1115 1120
 Leu Ala Leu Ile Thr Ala Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg
 1125 1130 1135
 Gln Tyr Lys Asp Met Met Ser Glu Gly Gly Pro Pro Gly Ala Gly Pro
 1140 1145 1150
 Gln

<210> 177
<211> 1364
<212> DNA
<213> Homo sapiens

<400> 177
 gccgaagagt tcacaagaatgtt gaagcttggaa agccggcggg tgccgcgttg taggaaaaggaa 60
 gcttaaacggc ttccagaaggcc ttgtccggagc tc当地gggttc ggaaagactta tc当地ccatgg 120
 aggccgcgttc ctggctgtgt ctgtctgtcc tgccgcgttg gcaaggctttt cc当地accgc 180
 cagaacccctt tgagctggac gatgtaaaggatt tccctgtcggt ctgtcaacttc tccggaaacctc 240
 agccgcgttg gtccaaaggcc ttccctgtgt tgctgtcgatgg agaggtggaa atccatggcc 300
 gcggcttcaa ctttagggcc gctgtatggc gcaaggccgaa cc当地ccggcgt 360
 atccgtacac ggtcaaggctt ctccggcgcc ggcggcgttcc acgtggggagcc gcaagggttc 420
 ctgtcgatgt actgttggcc gcccggcggt tgctgtcgatgg ctccggccctt aaggaaactgt 480
 ctgtcgaggaa cttaaagata accggcacca tgccctccgtt gcccctggaa gcaacaggac 540
 ttgcacgtttt ctaggtggcc ctacggcaacg tgctgtggcc gacaggggcggt tctgggttcg 600
 cc当地ggctca gcaaggccgttca accggggcc tcaaggactt gacatgttcc caaggacactt 660
 cgccgttccctt ttccggcgaa cagggttccgg ctttccggcc ctttaccagg cttagacccgt 720
 ctgacaatcc tggactggcc gaaacggccgac tgatgtggcc ttcttgttcc caacaggatcc 780
 cggccatcatcc gaaatcttggc ctggcaaca cagaatgttggaa gacggcccaaa ggccgttgcg 840
 cc当地ggctcc gggccggcgtt gtc当地ggcccc acggacttgc ctccggccac aactccgttc 900
 ggc当地ccatcc aaaccctttagt gctccggaggat gcatgtggccg caggccggctg aactccctca 960
 atccgtcggtt ctgtgggtttt gaaacgggtc taaaaggactt gcccggccaa ct当地ggatgt 1020
 tgc当地ggctca ctggcaacaagg ctggcaagggg cc当地ggccaggcc tgacggatgtg cccagggtgg 1080
 ataacccttgcg acgtggacgggg atacccttcc tggcccttttgg aactggccctt cccccagggg 1140
 gctccatgtaa ctggccggccgtt gtc当地ggccgttcc gacccctgtcc gtgggggttcc 1200
 cggggaaacctt gttgttgcgttcc caaggggccccc gggccctttgc ct当地ggatcca agacagaata 1260
 atggatgttgc acaaaatgtcc ttggcccttgc gggagttccgg tc当地ggatgtt gaggactttt 1320
 cc当地ggatcc aaccctttagt cccacccttttta taaaatctt aaac 1364

<210> 178
<211> 375
<212> PRT
<213> Homo sapiens

<400> 178
 Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Pro Leu Val His
 1 5 10 15
 Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
 20 25 30
 Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
 35 40 45

WO 2005/037989

PCT/US2003/024918

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt

Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
 50 55 60

Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
 65 70 75 80

Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
 85 90 95

Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
 100 105 110

Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile
 115 120 125

Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu
 130 135 140

Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp
 145 150 155 160

Leu Ala Glu Leu Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
 165 170 175

Ile Ala Gln Ala His Ser Pro Ala Phe Ser Cys Glu Gln Val Arg Ala
 180 185 190

Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
 195 200 205

Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
 210 215 220

Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
 225 230 235 240

Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
 245 250 255

Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
 260 265 270

Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
 275 280 285

Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
 290 295 300

Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
 305 310 315 320

Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr
 325 330 335

Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
 340 345 350

Ala Arg Ser Thr Leu Ser Val Gly Val Ser Gly Thr Leu Val Leu Leu
 355 360 365

Gln Gly Ala Arg Gly Phe Ala
 370 375

<210> 179
<211> 2633
<212> DNA
<213> Homo sapiens

<400> 179

ccgcggcaag aacatcccc tcgaggcagca gattacaatg ctgcaaacta aggatctcat 60
 ctggactttt tttttcctgg gaactgcagt ttctctgcag gtggatatttg ttcccgacca 120
 gggggagatc acgtttggag agtccaaattt ctctttatgc caatgtggcag gagatgcggc 180
 agataaagac atctccgggt tctcccccaa ttggaaaaag ctccacccaa accgcacgcg 240
 gatctcagtgt gtgtggaaatg atgttccctc tcaccaccc tcaccatctta acgcacacat 300
 cgatgacgcgt ggcatatcctc agtgtgtgtgt tacagcgcag gatggcagtgc agtccagg 360
 cacccgtcaac gtgaagatct ttccatgcgt catgttcacg aatgcgccaa ccccaacagg 420
 gtttccggag gggggaaatgt ccgtgtatgtt gtgtgtatgtgt gtccagctccc tccacccaa 480
 catccatctgg aaacacaaatgg ccggatgtgtt catcttgcataa aatggatgtcc gatcttataatg 540
 cctgtccaaa aactacttgc agatccgggg catcaagaaa acatgtggg gcacttattgc 600
 ctgtggggc agaatcttgg cttccgggg gatcaacttc aaggatccatc aggttcatgtt 660
 gaatgtggca cttatccatc gggccggca gatatttgcg atggccaccc ccaacctccg 720
 ccaggatccgtc accctttgtt ggcgtatccgca acggttccca gacggccacca tgatggcgc 780
 aaaggatgg gaacagatgg agcaagaggaa agacgtatgg aatgtacatctt tcacgcgacg 840
 tagtfcggcc ctggatccatca aaaaatgttgc taagaacggc gaggtgtatgtt acatctgtatc 900
 tgcgtggaaac aaggctggcg acggatgtgc gaccatccac ctcaaaatgtt ttgcacaaacc 960
 caaaaatcaca tatgtatgaa acaggatgtc catgtatggaa tggaggcagg tcaatcttac 1020
 ctgtgaagcc tccggagacc ccattccctc catcaccttgg aggacttcta cccggacat 1080
 cgacgacgaa gaaaagactc ttgtatggccca catgttgggtt ctttttttttcc 1140

```

<210> 180
<211> 848
<212> PRT
<213> Homo sapiens

<400> 180
Met Leu Gln Thr Lys Asp Leu Ile Trp Thr Leu Phe Leu Gly Thr
1          5          10          15
Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser
20          25          30
Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys
35          40          45
Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro
50          55          60
Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Ser Ser Ser Thr
65          70          75          80
Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
85          90          95
Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val
100         105         110
Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
115         120         125
Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser ser
130         135         140
Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145         150         155         160
Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
165         170         175
Arg Gly Ile Lys Lys Thr Asp Glu Gly Tyr Arg Cys Glu Gly Arg
180         185         190
Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile val
195         200         205
Asn Val Pro Pro Thr Ile Arg Ala Arg Gln Asn Ile Val Asn Ala Thr
210         215         220
Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Arg Phe
225         230         235         240
Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln
245         250         255
Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu
260         265         270
Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile
275         280         285
Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
290 Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu
295 300
305 Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile
310 315 320
325 Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu
330 335
340 Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser
345 350
355 Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile
360 365
370 Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu
375 380
385 Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr
390 395 400
405 Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro
410 415
420 Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser
425 430
435 Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu
440 445
450 Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr
455 460
465 Ala Val Asn Arg Ile Gln Glu Ser Phe Glu Phe Ile Leu Val Gln
470 475 480
485 Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser
490 495
500 Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val
505 510
515 Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gln Glu Glu Val
520 525
530 Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile
535 540
545 Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu
550 555 560
565 Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu
580 585 590
595 Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu
600 605
610 Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys
615 620
625 Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg
630 635 640
645 Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser
650 655
660 Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val
665 670
675 Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe
680 685
690 Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser
695 700
705 Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val
710 715 720
725 Ile Phe Val Leu Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu
730 735
740 Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys
745 750
755 Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala
760 765
770 Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu
775 780
785 Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn
790 795 800
805 Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys
810 815
820 Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys
825 830
835 Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
840 845

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10,207.655 Seq List Text 07.24.03.txt

<210> 181
<211> 1702
<212> DNA
<213> *Homo sapiens*

<210> 182
<211> 199
<212> PRT
<213> *Homo sapiens*

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

49076.00004pct2 10.207.655 Seq List Text 07.24.03.txt
195

<210> 183
<211> 1642
<212> DNA
<213> *Homo sapiens*

<210> 184
<211> 208
<212> PRT
<213> *Homo sapiens*

<400> 184
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
I 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75 80
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
115 120 125
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
130 135 140
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155 160
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser

DOI: 10.1007/s00339-007-0301-2

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
195 200 205

<210> 186
<211> 312
<212> PRT
<213> *Homo sapiens*

```

<400> 186
Met Ala Ala Gly Glu Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
      1          5          10         15
Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
      20         25         30
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
      35         40         45
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
      50         55         60
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
      65         70         75         80
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
      85         90         95
Ala Ala Leu Gln Arg Ser Leu Ala Ala Leu Ala Gln His Ser Val
      100        105        110
Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
      115        120        125
Leu Ala Asp Gln Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
      130        135        140
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
      145        150        155        160
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
      165        170        175
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Gly Val Lys Pro
      180        185        190
Pro Pro Pro Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
      195        200        205
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
      210        215        220

```

WO 2005/037989

PCT/US2003/024918

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
 225 230 235 240
 Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Gly Tyr
 245 250 255
 Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe
 260 265 270
 Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala
 275 280 285
 Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu
 290 295 300
 Thr Asp Pro Asn Gly Gly Leu Ala
 305 310

<210> 187

<211> 600

<212> DNA

<213> Homo sapiens

<400> 187

atggaaggcca gagacaagca ggtactccgc tccctgcgtc tggagctggg tgccgaggta 60
 ctggtggaa gactgttct tcagtaccc taccaggaa gaattttgc aaaaaaccac 120
 attcaagaaa tcaaaggctca aaccacaggc ctccggaaaga caatgcgtt gctggacatc 180
 ctgccttcga aggcccccaa agctttgc accttcccg attccctcca ggaaatttccc 240
 tgggtaagag aaagactgg aaggcgaga gggaaatgtca cagccgagct gcctacagg 300
 gactggatgg ccggaaatccc ctacacatc ctcagcagt cgcacatcaga ccagcagatt 360
 aaccaggctgg cttagaaactg aggccccgag tgggagccg tggtctgtc tctggactg 420
 tccccagccg acatctaccg ctgcaaggcc aacctatccc acaaactgtca ttccggatgt 480
 gtggaggcct ttgcccgtg gcgcacagt tttggggaaagc agggcacctt cctlaagttt 540
 caaaggggcc tccaggcagt ggaggctgtat ccctccctgc tccagcacat gctggagtga 600

<210> 188

<211> 199

<212> PRT

<213> Homo sapiens

<400> 188

Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu
 1 5 10 15
 Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln
 20 25 30
 Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Lys Ala Gln Thr
 35 40 45
 Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg
 50 55 60
 Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro
 65 70 75 80
 Trp Val Arg Glu Lys Leu Glu Lys Ala Arg Glu Glu Val Thr Ala Glu
 85 90 95
 Leu Pro Thr Gly Asp Trp Met Ala Gly Ile Pro Ser His Ile Leu Ser
 100 105 110
 Ser Ser Pro Ser Asp Gln Gln Ile Asn Gln Leu Ala Gln Lys Leu Gly
 115 120 125
 Pro Glu Trp Glu Pro Val Val Leu Ser Leu Gly Leu Ser Gln Thr Asp
 130 135 140
 Ile Tyr Arg Cys Lys Ala Asn His Pro His Asn Val His Ser Gln Val
 145 150 155 160
 Val Glu Ala Phe Val Arg Trp Arg Gln Arg Phe Gly Lys Gln Ala Thr
 165 170 175
 Phe Leu Ser Leu His Lys Gly Leu Gln Ala Val Glu Ala Asp Pro Ser
 180 185 190
 Leu Leu Gln His Met Leu Glu 195

<210> 189

<211> 1642

<212> DNA

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Homo sapiens

<400> 189
 ctctaaagggtcgggggtgg aatccttggg ccgcctggca agcgcggcaga cctggccagg 60
 gccagcgac cgaggacaga gggcgcacgg agggccggc cgacgcggcc gcccgttcga 120
 gaccggccgca tgagccccgtt ctgtgtctgt ctgcactcg tgcgttcccg ctgtcgagc 180
 agcgagctga ccgagctcaa gtctctatgc ctggggcgcg tggccaacgcg caagctggag 240
 cgcgtcgaga ccggccctaga ctctttccg atgcgtctcg agcagaacgcg cctggagccc 300
 gggcacaccg auctcttcgcg cgagctgtc gcctccctgc ggcgcacgcg cctgtcgccg 360
 cgctcgacg acttcgaggcg gggggccgcgc gccggggccg cctgtgggg aagaaagacct 420
 tggcgcacat ttaacatcat atgtataat gtggggaaat gtggggaaat attggagaaat gtgtggctgt 480
 Cagcttcaaaag ttccacagac caagatcgac acatcgagg acatcgagg acagatacc cgcacaaatcc 540
 acagacgcgtg tgccggaggc actyggaaatc tgaaaggatc acatcgagg acagatacc cgcacaaatcc 600
 gtggcccaacc tggtggggc tcttcggatcc tgccaggatca accttggtpgc tgacacttgta 660
 caagaggttc acgcattctac ctccggaaatcg agcaggatgtc gggccatgtc cccatgtca 720
 tggaaacttcg acgcattctac ctccggaaatcg tccgtatccg cgcgtcttt gcgttgggg 780
 accacaggcg tcttcggatccg tggactttg gtcttcggatccg gaaaggtagc ccaagctgt 840
 gaagaccccg caggaaggcga ggctgtatcg cgcacacgc accttgcattt gaactcaacgc 900
 tgcgtttt aatgcgttcc tcggcaccagg cggggcttgg gcccgtgcaca gatattttca 960
 ttcttcctc atatgcacat tgaccaatgcat ctgttcctca ctaaatggcgc tccgtcgccga 1020
 gtatgtggaa atgtggaaat gtgtccggac Cagaaggatc ctgtcgatgt gacgcgttcac 1080
 atgtgttactc cacagccggag gagacccgtt acatccctccca ggaatccggc gcaaggagag 1140
 aggtggagaaat ctggggatcc acatccctccca gagaatgttgc ctgtccatcc 1200
 gtggcgatctc ctggcccttc cagtggccgcg aacatggatgtt tttttttttt tcccttgggg 1260
 ccacccggac agacatgttgc actatggotca ggccgggtgc tggtgggggg agagatgtgg 1320
 ctggggfggg gttggggaaaat ctgggttgc ctgtggccatc ctcttggccc ctgtgtggat 1380
 tgatgttccct ctctggatact gtaatggatgg ggcgtatgtt gttggccaggaa cgaatttgaga 1440
 taatatctgtt gagggtgtca tgatgttgc acacacgcga ctctcttaaaat ctctctttgt 1500
 aggatttatgg gtcctggcaat tctacatgtt ctatgtttt tgatcaaaa tcaatctatcc 1560
 tctgatataaca gaattggccaa ggccggggaa tctctgtatct taaaagca gtcctttat 1620
 tccctaaatccat 1642

<210> 190

<211> 208

<212> PRT

<213> Homo sapiens

<400> 190

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
 1 5 10 15
 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
 20 25 30
 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
 35 40 45
 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
 50 55 60
 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
 65 70 75 80
 Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
 85 90 95
 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
 100 105 110
 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
 115 120 125
 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
 130 135 140
 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
 145 150 155 160
 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
 165 170 175
 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
 180 185 190
 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
 195 200

<210> 191

<211> 3492

<212> DNA

49076.000004pct2 10.207.655 seq List Text 07.24.03.txt
<213> Homo sapiens

<210> 192

<211> 4

<212> PRT

<213> Homo sapiens

<400> 192

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met
 1 5 10 15
 Cys Cys Ser Lys Cys Ser Pro Gly gln His Ala Lys Val Phe Cys Thr
 20 25 30
 Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr
 35 40 45
 Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys
 50 55 60
 Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg
 65 70 75 80
 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
 85 90 95
 Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly
 100 105 110
 Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys
 115 120 125
 Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
 130 135 140
 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met
 145 150 155 160
 Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly
 165 170 175
 Ala Val His Leu Pro Gln Pro Val ser Thr Arg Ser Gln His Thr Gln
 180 185 190
 Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
 195 200 205
 Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu
 210 215 220
 Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile
 225 230 235 240
 Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu
 245 250 255
 Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala
 260 265 270
 Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro
 275 280 285
 Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala ser Ala Leu Asp Arg
 290 295 300
 Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser
 305 310 315 320
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro
 325 330 335
 Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys
 340 345 350
 Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr
 355 360 365
 Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
 370 375 380
 Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr
 385 390 395 400
 Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly
 405 410 415
 Val Pro Asp Ala Gly Met Lys Pro Ser 420 425

<210> 193

<211> 1799

<212> DNA

<213> Homo sapiens

<400> 193

```

ccccacgcgttc cgcataaaatc agcacgcggc cggagaaccc cgcaatctct gccccacaa 60
aatacaccgca cgtatcgccca tcatactttaa gggtctgaac acacggggctt gagatcatat 120
aagagcgttc cttaccgcga tggaaacaacg gggacagaaac gcccccgccg cttcgggggc 180
ccggaaaaagg cacggcccgag gacccaggaa ggccgcgggaa gccaaggctcg ggctccgggt 240
ccccaaagacc ctttgtctcg ttgtcgccgc ggtcctgctcg ttgtgtctcg cttagtctgc 300
tctgtatcacc caacaagacc tagctccccca gcagagacgc gccccacaaac aaaagagggtc 360
cageccccca gagggtattgt gtcccccttg acaccatatac tcagaagacg gttagatgtt 420

```

<210> 19

<211> 41

<212> PRT

<213> Homo sapiens

<400> 194

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
 1 5 10 15
 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 20 25 30
 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60
 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 100 105 110
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 180 185 190
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 195 200 205
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
 210 215 220
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 225 230 235 240
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 245 250 255
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 260 265 270
 Ser Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 275 280 285
 Ile Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 290 295 300
 Pro Thr Glu Thr Leu Arg Gln Cys Phe ASP Asp Phe Ala Asp Leu Val

WO 2005/037989

PCT/US2003/024918

49076.000004pct2	10.207.655	Seq List Text	07.24.03.txt
305	310	315	320
Pro Phe Asp Ser Trp Glu	Pro Leu Met Arg Lys	Lys Leu Met Asp	
325	330	335	
Asn Glu Ile Lys Val Ala	Lys Ala Glu Ala Ala	Gly His Arg Asp Thr	
340	345	350	
Leu Tyr Thr Met Leu Ile	Lys Trp Val Asn Lys	Thr Gly Arg Asp Ala	
355	360	365	
Ser Val His Thr Leu Leu	Asp Ala Leu Glu Thr	Leu Gly Glu Arg Leu	
370	375	380	
Ala Lys Gln Lys Ile Glu	Asp His Leu Leu Ser	Ser Gly Lys Phe Met	
385	390	395	400
Tyr Leu Glu Gly Asn Ala	Asp Ser Ala Leu Ser		
405	410		

<210> 195

<211> 683

<212> DNA

<213> Homo sapiens

<400> 195

ggcttcagg aattccgcac	gagcttagct	gaagatgact	gacagtgtta	tttattccat	60
gttagatgtt	cctccggcaa	cccaaggcca	aaatggat	ggaccacagc	120
ctcttcagg	ccttcgttgtt	tttgccgtgt	ggcaaatgcgt	ttggggccttc	180
tcttcgtgtt	gtgtcgctat	accaggatgt	ttctgtccagg	ggctccaaact	240
tgccaggct	ccttagtgc	cagaccgtg	catggaaatgt	gtttaaccatt	300
ctcaggtag	gaaaaggact	ggaattctag	tctggaaatc	tgccctagcca	360
cctccgttg	ataaacggaca	atcaggaaat	gagccgtctc	caagttttcc	420
cttttgcgtg	attgtgtcg	ggaaacaattt	ttggctggagg	tggaaatgt	480
aaactctca	aggatttctt	ctaatacgctt	ttgtcgagaca	ttccgggtccca	540
tgttcttcaa	gcctcaacgt	gttgaatgtcc	tttacatcggt	ttgtgttaaga	600
ttagatagat	accactctgt	cttgaccctt	agatctgtca	tgtatcccta	660
gctggccact	ggctgttggg	aaa			683

<210> 196

<211> 189

<212> PRT

<213> Homo sapiens

<400> 196

Met Thr Asp Ser Val Ile Tyr Ser Met Leu Glu Leu Pro Thr Ala Thr					
1	5	10	15		
Gln Ala Gln Asn Asp Tyr Gly Pro Gln Gln Lys Ser Ser Ser Ser Arg					
20	25	30			
Pro Ser Cys Ser Cys Leu Val Ala Ile Ala Leu Gly Leu Leu Thr Ala					
35	40	45			
Val Leu Leu Ser Val Leu Leu Tyr Gln Trp Ile Leu Cys Gln Gly Ser					
50	55	60			
Asn Tyr Ser Thr Cys Ala Ser Cys Pro Ser cys Pro Asp Arg Trp Met					
65	70	75	80		
Lys Tyr Gly Asn His Cys Tyr Tyr Phe Ser Val Glu Glu Lys Asp Trp					
85	90	95			
Asn Ser Ser Leu Glu Phe Cys Leu Ala Arg Asp Ser His Leu Leu Val					
100	105	110			
Ile Thr Asp Asn Gln Glu Met Ser Leu Leu Gln Val Phe Leu Ser Glu					
115	120	125			
Ala Phe Cys Trp Ile Gly Leu Arg Asn Asn Ser Gly Trp Arg Trp Glu					
130	135	140			
Asp Gly Ser Pro Leu Asn Phe Ser Arg Ile Ser Ser Asn Ser Phe Val					
145	150	155	160		
Gln Thr Cys Gly Ala Ile Asn Lys Asn Gly Leu Gln Ala Ser Ser Cys					
165	170	175			
Glu Val Pro Leu His Trp val Cys Lys Lys Val Arg Leu					
180					

<210> 197

<211> 2967

<212> DNA

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 seq List Text 07.24.03.txt
<213> Homo sapiens

<400>	197	tagctccgcg	cgggggttc	ctcggtcct	tgtgttgc	gccgcgcag	ctgtgcgcg	60
		gggttttgtgg	gttgggttag	aggaggagct	gtcgcgac	ctgttagatc	ggttcttgg	120
		gcttttttttt	ctggggatgt	cttcattct	actgtcgatc	ctgtatccc	tgtctgg	180
		aggggatcccc	ccccggacac	tcggcaca	ggggatgc	ctttttttgc	caccatcc	240
		ttcgatcagg	atgttgaaaa	accaacccgc	ggatgtata	ctgtcgagg	ctggggcctc	300
		atttttttttt	tatgttgcata	atgttgcgt	tcgttcactg	gacttggaa	ttgtttttcg	360
		tcttttttttt	gaagaatgtta	cacaacaaat	cttcacgtg	ttttttttatc	ctatgcgg	420
		cttaggggg	gttgtatcca	ctgtggcaat	ttttttttatc	tagaaatgt	ttcaagatgt	480
		tttttttttt	atgtttttttt	ctgtttttat	aagggttcatc	ttttttttatc	ttttttttatc	540
		tcggcaatgt	tttttttttt	gacatgtat	ttttttttatc	atccacatgt	ttttttttatc	600
		tttttttttt	tttttttttt	taaaggaaaca	ttttttttatc	ttttttttatc	ttttttttatc	660
		gctggcagaa	aaaggcaaaa	aaaggccatgt	ttttttttatc	ttttttttatc	ttttttttatc	720
		tttttttttt	aaaggaaaaaa	aaaggaaaga	ttttttttatc	ttttttttatc	ttttttttatc	780
		cggccatgg	ccccccccc	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	840
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	900
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	960
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1020
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1080
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1140
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1200
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1260
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1320
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1380
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1440
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1500
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1560
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1620
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1680
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1740
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1800
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1860
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1920
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	1980
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2040
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2100
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2160
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2220
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2280
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2340
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2400
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2460
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2520
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2580
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2640
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2700
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2760
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2820
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2880
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2940
		tttttttttt	tttttttttt	ttttttttatc	ttttttttatc	ttttttttatc	ttttttttatc	2967

<210> 19

<211> 540

<212> PRT

<213> Homo sapiens

<400> 198

```

Met Pro Leu Phe Ala Thr Asn Pro Phe Asp Gln Asp Val Glu Lys Ala
1 5 10 15
Thr Ser Glu Met Asn Thr Ala Glu Asp Trp Gly Leu Ile Leu Asp Ile
20 25 30
Cys Asp Lys Val Gly Gln Ser Arg Thr Gly Pro Lys Asp Cys Leu Arg
35 40 45
Ser Ile Met Arg Arg Val Asn His Lys Asp Pro His Val Ala Met Gln
50 55 60
Ala Leu Thr Leu Leu Gly Ala Cys Val Ser ASN Cys Gly Tyr Ile phe

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 His Leu Glu Val Cys Ser Arg Asp Phe Ala Ser Glu Val Ser Asn Val
 70 75 80
 85 90 95
 Leu Asn Lys Gly His Pro Lys Val Cys Glu Lys Leu Lys Ala Leu Met
 100 105 110
 Val Glu Trp Thr Asp Glu Phe Lys Asn Asp Pro Gln Leu Ser Leu Ile
 115 120 125
 Ser Ala Met Ile Lys Asn Leu Lys Glu Gln Gly Val Thr Phe Pro Ala
 130 135 140
 Ile Gly Ser Gln Ala Ala Glu Gln Ala Lys Ala Ser Pro Ala Leu Val
 145 150 155 160
 Ala Lys Asp Pro Gly Thr Val Ala Asn Lys Lys Glu Glu Glu Asp Leu
 165 170 175
 Ala Lys Ala Ile Glu Leu Ser Leu Lys Glu Gln Arg Gln Gln Ser Thr
 180 185 190
 Thr Leu Ser Thr Leu Tyr Pro Ser Thr Ser Ser Leu Leu Thr Asn His
 195 200 205
 Gln His Glu Gly Arg Lys Val Arg Ala Ile Tyr Asp Phe Glu Ala Ala
 210 215 220
 Glu Asp Asn Glu Leu Thr Phe Lys Ala Gly Glu Ile Ile Thr Val Leu
 225 230 235 240
 Asp Asp Ser Asp Pro Asn Trp Trp Lys Gly Glu Thr His Gln Gly Ile
 245 250 255
 Gly Leu Phe Pro Ser Asn Phe Val Thr Ala Asp Leu Thr Ala Glu Pro
 260 265 270
 Glu Met Ile Lys Thr Glu Lys Lys Thr Val Gln Phe Ser Asp Asp Val
 275 280 285
 Gln Val Glu Thr Ile Glu Pro Glu Pro Glu Pro Ala Phe Ile Asp Glu
 290 295 300
 Asp Lys Met Asp Gln Leu Gln Met Leu Gln Ser Thr Asp Pro Ser
 305 310 315 320
 Asp Asp Gln Pro Asp Leu Pro Glu Leu Leu His Leu Glu Ala Met Cys
 325 330 335
 His Gln Met Gly Pro Leu Ile Asp Glu Lys Leu Glu Asp Ile Asp Arg
 340 345 350
 Lys His Ser Gln Leu Ser Glu Leu Asn Val Lys Val Met Glu Ala Leu
 355 360 365
 Ser Leu Tyr Thr Lys Leu Met Asn Gln Glu Asp Pro Met Tyr Ser Met Tyr
 370 375 380
 Ala Lys Leu Gln Asn Gln Pro Tyr Tyr Met Gln Ser Gly Val Ser
 385 390 395 400
 Gly Ser Gln Val Tyr Ala Gly Pro Pro Pro Ser Gly Ala Tyr Leu Val
 405 410 415
 Ala Gly Asn Ala Gln Met Ser His Leu Gln Ser Tyr Ser Leu Pro Pro
 420 425 430
 Glu Gln Leu Ser Ser Leu Ser Gln Ala Val Val Pro Pro Ser Ala Asn
 435 440 445
 Pro Ala Leu Pro Ser Gln Gln Thr Gln Ala Ala Tyr Pro Asn Thr Met
 450 455 460
 Val Ser Ser Val Gln Gly Asn Thr Tyr Pro Ser Gln Ala Pro Val Tyr
 465 470 475 480
 Ser Pro Pro Pro Ala Ala Thr Ala Ala Ala Thr Ala Asp Val Thr
 485 490 495
 Leu Tyr Gln Asn Ala Gly Pro Asn Met Pro Gln Val Pro Asn Tyr Asn
 500 505 510
 Leu Thr Ser Ser Thr Leu Pro Gln Pro Gly Gly Ser Gln Gln Pro Pro
 515 520 525
 Gln Pro Gln Gln Pro Tyr Ser Gln Lys Ala Leu Leu
 530 535 540

<210> 199

<211> 2531

<212> DNA

<213> Homo sapiens

<400> 199

tctaaatgtt atctttggaaa ttccagataga tactcatcct acctgaaat aaactgagat 60
aaatccatgtt aagaatgtt agttaattct acataaagt ctatcattga ttcttcttgg 120

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

tggtaaaaat cttagttcat gtgaagaat ttcatgtaa tgtttagct atcaaaccg 180
actgtcacct actcgtgcac aaaactgcct cccaaagact ttcccagggt cccgtatc 240
aaacattaaat gaggataatq gaagatagca cgtatctgtc agatttgaga aacagccaa 300
aacaaaaaat gaagtatgac tttccctgtg aacttcacag aatgttcaca tattcaactt 360
tccccccgg ggtgcgtgc tcagaaaaaa gcttgcgtg tgctgggtt tattatactg 420
gttgtaatgc caaggctcaa tgcttctgtt gtggcgtat gctggataac tgaaactag 480
gagacagtcc tattcaaaag cataaaccgc tatatccctag cttagctttt attcagaatc 540
tggttcagc tagtctggg tccaccctct aqaatacgct tccaatgaga aacagttt 600
cacattcat atctccccc tggaaacata sttagctgtt cagttgttct tactccgc 660
ttttcccaa ccctcttaat tctagagcag tgaaagacat ctcttcatcg aggataacc 720
cctacagtt tycatgtatc tgaaagaat gatgttgc gactgtgtt ttattatata gacccgtgg 840
taactttttt gtcacccatca gatgttgc gactgtgtt ttattatata gacccgtgg 840
atagggtac ctgtttttc tggtgtggg gactcgatgg ctgggaaacc aaggatgtt 900
ctatgcac acaccgggg cattttccca atcttcgtt cttttttttt tttttttttt 960
ctctgggtt tagatcttc aatctgcgtc tgccagatca tgccagatca tgccagttc 1020
ttatgtactg gccatctgtt tgccagatca tgccagatca tgccagatca tgccagatca 1080
attatgttgg tgccatgtt gatgttcaat gttttttttt tgatgttggc tgatgttgg 1140
ggaaatctgg agatgtatca tggtgttgg gatgttcaat gttttttttt tgatgttgg 1200
tgatgtcaat gaaagccaa gatgttggt tgatgtatca tgccagatca tgccagatca 1260
ttgaacacgtt tggttcaact tgatgttcaat tgccagatca tgccagatca tgccagatca 1320
ttccattingg acctggggaa agtctttccatc tgatgtatca tgccagatca tgccagatca 1380
ttaaatctgc ttggggaaat ggcttttataa gatgttcaat gaaacaaacaa tgatgttgg 1440
aaatctgcg aactggggaa agtactaaaaa ctgttataa tattttttt tgatgttgg 1500
atgttggaa tgaaaaaaatc gaggaggaga agggaaaaaaa agtggaaagaa atggccatcg 1560
atgttggtcc attaaatcc gaaacacatc tggttccatc tgccagatca tgccagatca 1620
ttccatccatc tgatgttcaat tgccagatca tgccagatca tgccagatca tgccagatca 1680
ttaaacaaaaa aacacatca ctttataaag cgagaaaaat gattgtatcc attttttttt 1740
aaggaaatgtc tgccacccat atcttcaaaa actgttcaat gaaatgttcc tgatgttgg 1800
ataagaacctt attttgttat gaaatataa agatattcc acacaaaaat gttttttttt 1860
tgtactggaa agaaacatgg aggagggttc aagaaacacg acttggtaaa tgatgttgg 1920
acaaaaatgtc ttgttgcata tttttttttt tggttgcattc tgatgtatcc tgccagatca 1980
cccccttcctt aaaaaaaaaa ctatgttcaat ggggttataat caagggtact tgatgttgg 2040
ttctcttta aaaaaaaaaa tgatgttcaat tttttttttt tgatgttggc tgatgttgg 2100
ttgttgcata tgaaacactc taaggaaaaaa agggatgttcaat gatgttggc tgatgttgg 2160
ttcatgttct agtctgtttt tgatgttcaat atcttgcattc tgccagatca tgccagatca 2220
tttaacttca atcttgcattc tgatgttcaat tgccagatca tgccagatca tgccagatca 2280
tgatgttgcattc tgatgttcaat tgccagatca tgccagatca tgccagatca tgccagatca 2340
attttttttt ttgttgcata tgatgttcaat tgccagatca tgccagatca tgccagatca 2400
ccaaagactc tgggatgttcc tgatgttcaat tgccagatca tgccagatca tgccagatca 2460
gtgtttttt aaatgttcaat tgccagatca tgccagatca tgccagatca tgccagatca 2520
taaagtgtct tttttttttt tgcccccattc tgccagatca tgccagatca tgccagatca 2531

```

<210> 200

<211> 618

<212> PRT

<213> Homo sapiens

<400> 200

```

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
1 5 10 15
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
20 25 30
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
35 40 45
Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
50 55 60
Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
65 70 75 80
Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
85 90 95
Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
100 105 110
Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr
115 120 125
Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu
130 135 140
His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro
145 150 155 160
Leu Asn Ser Arg Ala Val Glu Asp Ile Ser Ser Ser Arg Thr Asn Pro

```

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Tyr Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe Leu Thr Tyr His
 165 170 175
 180 185 190
 Met Trp Pro Leu Thr Phe Leu Ser Pro Ser Glu Leu Ala Arg Ala Gly
 195 200 205
 Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala cys Gly
 210 215 220
 Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp Ala Met Ser Glu His
 225 230 235 240
 Arg Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Glu Thr
 245 250 255
 Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Ala Arg
 260 265 270
 Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu
 275 280 285
 Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp Asp Val
 290 295 300
 Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser Gly Asp
 305 310 315 320
 Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu Phe Leu
 325 330 335
 Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile Gln Gly Arg Tyr
 340 345 350
 Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Thr Thr Gly Glu
 355 360 365
 Glu Asn Ala Asp Pro Pro Ile Ile His Phe Gly Pro Gly Glu Ser Ser
 370 375 380
 Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
 385 390 395 400
 Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Glu Ser Lys
 405 410 415
 Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
 420 425 430
 Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Lys Glu Lys
 435 440 445
 Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
 450 455 460
 Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
 465 470 475 480
 Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
 485 490 495
 Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
 500 505 510
 Ile Leu Val Lys Gly Asn Ala Ala Asn Ile Phe Lys Asn Cys Leu
 515 520 525
 Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
 530 535 540
 Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
 545 550 555 560
 Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
 565 570 575
 Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val cys
 580 585 590
 Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile
 595 600 605
 Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
 610 615

<210> 201
<211> 2477
<212> DNA
<213> *Homo sapiens*

<400> 201
atggcagacg cggctccatg cggtatgggtg ctatgtttag gcggttgtag aagttaataa 60
aggatccat ggagaacact gaaaaactcg tggatcaaa atccattaaa aattttggAAC 120
aaatggatcat acatggaaacg gaaatcgtt acttcgtttag atccctgtttt aacatgttataa 180
aatatggatata tccttqatggat qttttttttttttaataatattaa taaaatggat aatccatgttataa 240

<210> 202

<211> 277

<212> PRT

<213> Homo sapiens

<400> 202

```

Met Glu Ash Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
      5          10          15
Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
      20          25          30
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
      35          40          45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
      50          55          60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Gly Thr Phe Arg Asn
      65          70          75          80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
      85          90          95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
      100         105         110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
      115         120         125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
      130         135         140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
      145         150         155         160
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
      165         170         175
Gly Val Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
      180         185         190

```

See *Notes*, page 40, note 2.

WO 2005/037989

PCT/US2003/024918

```

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
   195          200          205
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
   210          215          220
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
   225          230          235          240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
   245          250          255
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
   260          265          270
Leu Tyr Phe Tyr His
   275

```

<210> 20

<211> 1906

<212> D

<213> Homo sapiens

<400> 203

<210> 20

<211> 613

<212> PRT

<213> Homo sapiens

<400> 204

Met	Phe	Arg	Cys	Gly	Gly	Leu	Ala	Ala	Gly	Ala	Leu	Lys	Gln	Lys	Leu	
				5						10				15		
1	Val	Pro	Leu	Val	Arg	Thr	Val	Cys	Val	Arg	Ser	Pro	Arg	Gln	Arg	Asn
					20				25					30		
Arg	Leu	Pro	Gly	Asn	Leu	Phe	Gly	Arg	Trp	His	Val	Pro	Leu	Glu	Leu	
					35			40					45			
Gln	Met	Thr	Arg	Gln	Met	Ala	Ser	Ser	Gly	Ala	Ser	Gly	Gly	Lys	Ile	
					50			55				60				
Asp	Asn	Ser	Val	Leu	Val	Leu	Ile	Val	Gly	Leu	Ser	Thr	Val	Gly	Ala	
					65			70				75				

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn
85 90 95
Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys
100 105 110
Ala Ala Leu Ser Ala Ser Glu Gly Glu Glu Val Pro Gln Asp Lys Ala
115 120 125
Pro Ser His Val Pro Phe Leu Ile Gly Gly Gly Thr Ala Ala Phe
130 135 140
Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu
145 150 155 160
Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser
165 170 175
Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Leu Arg
180 185 190
Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro
195 200 205
Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly
210 215 220
Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Cys
225 230 235 240
Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys
245 250 255
Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg
260 265 270
Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly
275 280 285
Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr
290 295 300
Ile Ile Gly Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly
305 310 315 320
Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu
325 330 335
Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr
340 345 350
Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile
355 360 365
Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys
370 375 380
Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu
385 390 395 400
Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser
405 410 415
Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn
420 425 430
Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly
435 440 445
Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu
450 455 460
Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser
465 470 475 480
Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly
485 490 495
Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr
500 505 510
Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile
515 520 525
Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Glu Ile Thr Ile Pro
530 535 540
Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr
545 550 555 560
Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile
565 570 575
Val Leu Trp Asp Ile Phe Asp Arg Met Pro Ile Ala Arg Lys Ile Ile
580 585 590
Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu Val Ala Lys Leu Phe
595 600 605
Asn Ile His Glu Asp
610

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 206
<211> 91
<212> PRT
<213> *Homo sapiens*

```

<400> 206
Met Ala Ala Asp Arg Gly Arg Arg Ile Leu Gly Val Cys Gly Met His
      5          10          15
Pro His His Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
      20          25          30
Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
      35          40          45
Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
      50          55          60
Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
      65          70          75          80
Ala Phe Asp Ala Phe Cys Glu Ala Leu His Ser
      85          90

```

<210> 207

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 207

tctgtatccgg agccccaaatc tggtacaaa actcacatc gcccacccgtt cccacgcact 60
 gaacctttcgat ggaaaaacccgtt agtttccttc ttccccccat aaccacaaaggta cacccttcgtat 120
 atcccttccggat cccttgggggtt acatgtttccat gtgtggggacca tgaggccacca agaccatcgag 180
 tcggaaatggat ctggggatgtt acgggtttttt gggatggggatc atgcacaaatc aaaggccgggg 240
 gaggaggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 300
 tggtttttttttt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 360
 gaaaaatggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 420
 atccatccggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 480
 attcggatccggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 540
 tattccggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 600
 accggccatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 660
 gacaatggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 720
 caaacatccggatgtt gggggggggggt gggggggggggt gtcacgttttccatc acggccctccatc 780
 ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt 840
 ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt 900
 ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt ggggggggggggtt 960

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 208
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 208

Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1 5 10 15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
20 25 30
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
50 55 60
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65 70 75 80
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
85 90 95
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
100 105 110
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
115 120 125
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
130 135 140
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145 150 155 160
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
165 170 175
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
180 185 190
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
195 200 205
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
210 215 220
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235

<210> 209
<211> 718
<212> DNA
<213> Artificial sequence

<220>
<223> Fusion polynucleotide

<221> misc_feature
<222> 34, 43, 52, 55, 58, 64
<223> n = A,T,C or G

<400> 209

tgatcaagaa ccacatggag gatgcacgtg cccnacgtgc ccncaatgcc cngcncnnga 60
acthccaggaa ggcccttcgt tctttgttcc cccccccgaa 100
cccaaggacgc tccttcattc 120
tttgaggaggc cgagtacgtg cgcgtttagt ggacgtcgaa 140
tttcaactcg tatattgtg gcgttgtgggtt ggcgaacggcc 160
aatacgaagc caaaagaggaa 240
acagttcaac agcacgtacc gcgtgtggtag cgtcttcgc 300
gacggggaga gaattcaagt gcaaggctcgaa caacaacagt ctccccggccc ctaetcgag 360
gaccatctcc aaggcccaaag ggcacagcccc ggagccgcag 420
cgccggaaaga ctggcccaagg acacgttgag ctgttacatgc 480
agtcacatc aacgttgatg ggcagagggaa cggtcagccg 540
caacacgcgc ccacagctgg acaacgcggc gcacctacttc 600
ggaaaaagac acgtggccagc gggggagaaac cttaaacctgt tggtgtatgc atgaggccct 660
gcacaacacc tacacccaga aatccatcgc ccagtcttcg 718
ggttaaatagt aatctaga

<210> 210
<211> 757

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 210	tgtcaaaaga	ccaagacac	caaaccaca	accacaacca	caaccacaac	ccaaatctac	60
	aacagatcc	aagtgtccc	aatgttcaggc	ccctggatctc	ctggggggc	cctcgtt	120
	cattttcccc	ccgaaaccca	aggactgcct	tccttcattt	ggggggcc	aggcttcgtg	
	cgttgttgc	gacatggggc	aggaaacggcc	cgagggtcagt	ttaacttgtt	acatttggtt	240
	cgtgttcgg	cgaaacggcc	acacggggcc	aaaaggggg	gttttttttt	gcatcttcc	300
	cgtgttcaggc	gttcggccca	tccggaccca	gaactgggtt	acggggaa	attttttttt	
	caagggtttt	aacaaaggctc	tccggccccc	catcgagaa	accatcttca	aggccaaagg	420
	cgacggccgg	gaggcccgagg	tgatccatct	ggggccccac	cgggggaa	tggccaaagg	
	caccgttgc	gttacatcgcc	tggttcaaaag	tttttttttt	cctgtatata	acgttgtatgt	540
	cgagaggat	gggcggccgg	atgtacgggg	catacgtttt	accacccca	ccatcggtgg	600
	caacgacggg	actttttttt	tttttttttt	tttttttttt	ggaaatggaa	cttgcggcc	
	ggggggaaacc	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	
	attttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	

<210> 211

<211> 727

<212> DNA

<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<210> 212

<211> 231

<212> PRT

<213> Artificial Sequence

<220>
<223> Fusion polypeptide

```

<400> 212
Ile Pro His Gly Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu
      1           5          10          15
Pro Gly Gly Pro Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val
      20          25          30
Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp Val
      35          40          45
Gly Lys Glu Asp Pro Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val
      50          55          60
Glu Val Arg Thr Ala Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
      65          70          75          80
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
      85          90          95
Thr Gly Lys Lys Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
      100         105         110
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
      115         120         125

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
130 135 140
Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn
145 150 155 160
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
165 170 175
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
180 185 190
Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr
195 200 205
Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
210 215 220
Ile Thr Gln Ser Ser Gly Lys
225 230

<210> 213

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 213

Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln
1 5 10 15
Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
20 25 30
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
35 40 45
Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp
50 55 60
Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
65 70 75 80
Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
85 90 95
Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
100 105 110
Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
115 120 125
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
130 135 140
Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
145 150 155 160
Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
165 170 175
Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
180 185 190
Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
195 200 205
Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
210 215 220
Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
225 230 235 240
Ser Ile Thr Gln Ser Ser Gly Lys
245

<210> 214

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 214

Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
1 5 10 15
Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
20 25 30
Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
35 40 45
Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp
50 55 60
Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
65 70 75 80
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
85 90 95
His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
100 105 110
Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
115 120 125
Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
130 135 140
Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
145 150 155 160
Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gln Gln Pro Glu Ser
165 170 175
Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
180 185 190
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
195 200 205
Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
210 215 220
Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
225 230 235

<210> 215

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Fusion polynucleotide

<400> 215

gatcaggagc ccaaattcttg tgacaaaact cacacatgcc cacccgtgcc agca

54

<210> 216

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 216

Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15
Pro Ala

<210> 217

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 217

gatctggagc ccaaattcttg tgacaaaact cacacatgcc cacccgtgcc agca

54

<210> 218

WO 2005/037989

PCT/US2003/024918

<211> 18 49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 218

Asp	Leu	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
1				5				10					15		
Pro	Ala														

<210> 219

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 219

cctgaacctc	tggggggacc	gttcagttcc	cttttcccc	caaaacccaa	ggacacccct	60
atgatctccc	ggaccccttg	ggtcacatgc	gtgggttgtgg	acgtgagcca	cgaagaccct	120
gaggtaaagt	tcaactgtt	Cgtggacggc	gtggagggtgc	ataatgccaa	gacaaggccg	180
cgggaggaggc	agtacaacag	cacgttacgt	gtggtcagcg	tcctcacccgt	cctgcacccag	240
gactggtctgt	atggcaagga	gtacaatgtc	aagggtctcca	acaacggccct	ccagcccccc	300
atcgaaaaaa	ccatctccaa	agccaaa				327

<210> 220

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 220

Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
1				5				10				15			
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	val	Thr	cys	Val	Val
				20				25				30			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
				35				40				45			
Asp	Gly	Val	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
				50				55			60				
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				65				70			75			80	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
				85				90			95				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys			
				100				105							

<210> 221

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 221

ggccggcccc	gagaaccaca	ggtgtacacc	ctggccccc	cccgggagga	gatgaccaag	60
aaccaggatc	gcctggaccc	cctgttgtatc	ggcttcttatc	ccaggcgacat	cccccgtgg	120
tggggagaca	atggggaccc	ggagaacaaac	tacaagacca	cgccctccgt	gtggggactcc	180
gaccgtctct	tctttctctta	tagcaagctc	accgttgacca	agagcagggt	gcagcagggg	240
aacgttcttc	catgtcccg	gtatgtatcg	gttttttttt	accactacac	gcagaagagg	300

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt 324
ctctccctgt ccccggtaa atga<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence<220>
<223> Fusion polypeptide<400> 222
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105<210> 223
<211> 54
<212> DNA
<213> Artificial Sequence<220>
<223> Fusion polynucleotide<400> 223
gatcaggagc ccaaattttc tgacaaaact cacacatccc caccgtcccc agca 54<210> 224
<211> 18
<212> PRT
<213> Artificial Sequence<220>
<223> Fusion polypeptide<400> 224
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1 5 10 15
Pro Ala<210> 225
<211> 712
<212> DNA
<213> Artificial Sequence<220>
<223> Fusion polynucleotide<400> 225
tgatcacccc aaatcttctg acaaaaactca cacatctcca cgtcctcag cacctgaact 60
cctgggtgta ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgtatctc 120
ccggaccctt gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctggaggtaa 180
gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaagac cgcggggagga 240

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 gcagttacaa acgacgtacc gtgttgtcag cgtccctacc gtccgtcacc aggactggct 300
 gaatggcaag gactacaagt gcaagggtc tc caacaaggcc ctcccagcccc ccatcgaaaa 360
 aacaatcttc aaaggccaaag ggccggccccc agaaccacag gtgtacaccc tgcggccatc 420
 ccgggtatgg ctgaccaaga acccagggtcag ctggacactgc ctggtaaaag gtttctatcc 480
 caggcacatc gcccgtggat gggagagcaat tgccggccgg gagaacaact acaaagaccac 540
 gcctccctgt ctggactccg acggctccctt ctggacttcac agcaagctca cctggacaa 600
 gagcagggtgg cagcaggggga acgtcttc atgctccgtg atgcgtgagg cctcgacaaa 660
 ccactacacg cagaagagcc tctccctgtc tccggtaaa tgataatcta ga 712

<210> 226

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 226

Asp His Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1 5 10 15
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 20 25 30
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 35 40 45
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 50 55 60
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 65 70 75 80
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 85 90 95
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 100 105 110
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 115 120 125
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 130 135 140
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 145 150 155 160
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 165 170 175
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 180 185 190
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 195 200 205
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 210 215 220
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 227

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer for llama IgG1 constant region

<400> 227

gttgttgcataagaaccaca tggaggatgc acgtg

35

<210> 228

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

<223> 5' primer for llama IgG2 constant region

<400> 228
qtttgtgatc aagaacccaa gacaccaaaa cc

32

<210> 229
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for llama IgG3 constant region

<400> 229
gttgttgcatc aagcgccacca cagcgaagac ccc

32

<210> 230
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Llama Fc sense sequencing primer

<400> 230
ctqaqatcqa qttcaqctq

19

<210> 231
<211> 19

<212> DNA
<213> Artificial sequence

<220>
<223> Llama Fc antisense sequencing primer

<400> 231
cctcctttqq ctttqtctc

19

<210> 232
<211> 1527

<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<221> misc_feature

<222> 843, 852, 861, 864, 867, 873
<223> n = A,T,C or G

<400> 232

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

<210> 233

<211> 1566

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 233

```

aaggatccggc ccatggattt ttcactgcg attttcaact ctcgttcaat cagtgttcca 60
gtcataatgg ccaggagaca aatttgtctc tcccgttc cagaacctt gtcgtatctt 120
ccaggggaga aggttcacaa gacttgcggg cgcgttcaa gtgttaattt catgtacgg 180
taccacgaga agccggatc ttcccccaaa ctggcttttt atggccatcc caactcggt 240
ttggatgtcc ctgttcgtttt cttggcgatc gggttctgggg ctcttactt ttcataactt 300
agcaggatgg aggttcacaa gttgcggatc tattatccgg agactgggg tttaaaccc 360
ccccatggcc gtgtgggggg caatgttcggg ctggaaatgg ggcgttggtt gggcgttgggt 420
ggatctgggg ggggtggggg ctttccggct tttttttttt agtgcgttgggg tgacgttgggt 480
aggctggggg cttccatggg gatgttcgtc aaggcttcgtt gtcataccattt taccatgtt 540
aatatgtcact ggtttaaaacca gacccatggc gggccgtttt aatggattttt agcttatatt 600
ccaggaaatgg tgatgtatcc ttcaaaatccg aatgttcgtt gcaaggccac agactgttgg 660
gacaataatcc ccacggacac ttcatgttcg cttcagccgg tgcatacttga agactgttggc 720
ttgtttatcc ttgttcacaa ggtttttttt tttttttttt actgttactt cgtatgttgg 780
ggcacaagggg ccacgggttc acgtttttttt gttttttttt ccaaggacactt aaaaaaccaaa 840
ccacaacaaac accatccaaa ttatccatca adaaatccca agttgttccaa atgttcaccc 900
ttcgatgtcc tggggggggg cttagtttc atttttttttt cttttttttt gggacgttcc 960
ttccatgtttt gggggggggg ggttcgttgc ttgtttttttt agtgcgttggcc ggaatggccc 1020
ggatgttgggg aatggggggg gttttttttt tttttttttt ggtttttttt gggggggggg 1080
aaaggagggaa agtttcacaaac cttttttttt tttttttttt ggtttttttt gggggggggg 1140
ggatgttgggg aatggggggg gttttttttt tttttttttt ggtttttttt gggggggggg 1200
atccggaaaga cttttttttt tttttttttt ggtttttttt ggtttttttt gggggggggg 1260
ggcccccaccc gggaaagggtt gggggggggg acgtttttttt tttttttttt ggtttttttt 1320
ttcttccaccc ctgtatccaa cttttttttt tttttttttt ggtttttttt ggtttttttt 1380
aytacccatgg ccacccggcc acgtttttttt tttttttttt ggtttttttt ggtttttttt 1440
ctctcggttcc gaaadacaaa gttttttttt tttttttttt ggtttttttt ggtttttttt 1500
gaggccgttcc acacccactt cttttttttt tttttttttt ggtttttttt ggtttttttt 1560
ttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1620

```

<210> 234

<211> 1536

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 234

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ccaggaaatg gtgatacttc ctacaatcg aagttciaagg gcaaggccac actgactgtg 660
 gacaaaatccc ccagcacagc ctatcatcgag ctcagccgg tgacatcttg agactcttgtc 720
 gcttatrttc qtgcagaqagt gotgactatc agtaactttt actggatctt ctgtgtctgg 780
 ggacacaggga ccacgggtcac cgttcttctt gatcaagcga accacagcga agacccaggc 840
 tccaaatgttc ccaaaggcccccc accggccctaa cttctttaggg ggcacccgggtt ctcatcttc 900
 ccccccggaaag ccaaggaaacgt cttctccatc accggaaaaac ctgagggtcac gtgcttgggg 960
 tggacgtgggg taaaaggaaacg cttgagatcg agttaacgct gtccctgtgg tgacacagag 1020
 gtacacacgg cttgagacaaa gccaaaggag gaacagttca acagacgtta cccgggtgttc 1080
 agcgtctcgcc ccatcccgagca ccaggactgg ctgacgggggg aggaatttca gtcgaaggtc 1140
 aacaacadaag ctatcccgagc cccatcgagc agggaccatc ccaggccca aggccggaccc 1200
 cggggaggccgc aggtgttacac cttggcccca caccggggaa ggcacccgtg 1260
 agcgttaacctt gcttgggttcaaa aggttttttc ccagggttaca tcacgttgg tggtggagggg 1320
 aatggggccgc cggagtccaga gggccacttc gccaacacgcg ccccacagct ggacaaacgac 1380
 gggacccatctt cttcttacatc caaactttcc ttggggaaaacg acacgttggca ccaggggggaa 1440
 gttttccactt gtgttggatg gcacgggtctt ctacaaatc actccacccca gaaatccatc 1500
 acccaggatcc cgggttataata gtaatcttggcc 1536

<210> 235

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 235

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Gln Pro His Gly
 260 265 270
 Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu Pro Gly Gly Pro
 275 280 285
 Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Phe
 290 295 300
 Gly Gly Arg Val Thr Cys Val Val Val Asp Val Gly Lys Lys Asp Pro
 305 310 315 320
 Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val Glu Val Arg Thr Ala
 325 330 335
 Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 340 345 350
 Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe
 355 360 365
 Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr
 370 375 380
 Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu
 385 390 395 400
 Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys
 405 410 415
 Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn Val Glu Trp Gln Arg
 420 425 430
 Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln
 435 440 445
 Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly
 450 455 460
 Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr Cys Val Val Met His
 465 470 475 480
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser
 485 490 495
 Gly Lys

<210> 236
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 236
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Thr
 260 265 270
 Pro Lys Pro Gln Pro Gln Pro Gln Pro Asn Pro Thr Thr Glu
 275 280 285
 Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

290	295	300
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Ser Gly		
305	310	315
Arg Pro Glu Val Thr Cys Val Val Val Asp Val Gly Gln Glu Asp Pro		
325	330	335
Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly Ala Glu Val Arg Thr Ala		
340	345	350
Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val		
355	360	365
Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe		
370	375	380
Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
385	390	395
Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu		
405	410	415
Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys		
420	425	430
Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Asn Val Glu Trp Gln Arg		
435	440	445
Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Thr Thr Pro Pro Gln		
450	455	460
Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly		
465	470	475
Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe Thr Cys Val Val Met His		
485	490	495
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser		
500	505	510
Gly Lys		

<210> 237

<211> 503

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 237

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser		
1	5	10
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile		
20	25	30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser		
35	40	45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser ser		
50	55	60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro		
65	70	75
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile		
85	90	95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp		
100	105	110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys		
115	120	125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser		
130	135	140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala		
145	150	155
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr		
165	170	175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile		
180	185	190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe		
195	200	205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr		
210	215	220
Met Gln Leu Ser Ser Leu Thr Ser Gln Glu Asp Ser Ala Val Tyr Phe Cys		

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 225          230          235          240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Val
 245          245          250          255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ala His Ser His
 260          265          265          270
Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys Pro Gly Pro Glu Leu
 275          280          285          285
Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro Lys Ala Lys Asp Val
 290          295          300          300
Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys Leu Trp Trp Thr Trp
 305          310          315          320
Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp Ser Val Asp Asp Thr
 325          330          330          335
Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
 340          345          345          350
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
 355          360          365          365
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
 370          375          380          380
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
 385          390          395          400
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Leu Ala Lys Asp Thr
 405          410          415          415
Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe Pro Ala Asp Ile Asn
 420          425          430          430
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
 435          440          445          445
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
 450          455          460          460
Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Val Phe Thr
 465          470          475          480
Cys Val Val Met His Glu Ala Leu His Asn His Ser Thr Gln Lys Ser
 485          490          495          495
Ile Thr Gln Ser Ser Gly Lys
 500

```

<210> 238

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-primer for llama IgG1, IgG2, IgG3 constant region

<400> 238

gttggtttctta gattacttatt taccggaaaga ctggggtgatg ga 42

<210> 239

<211> 1521
232 RNI

<212> DNA
<213> Artificial Sequence

-220-

<223> fusion polynucleotide

<400> 239

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 gacaatcc ctacatcgag ctcagcagg tgcacatctga agacttcggc 720
 gtcattttctt gtgcagaagg ggtgtactat agtaactt actggactt cgtatgtgg 780
 ggccaggaga ccacggtcac cgtctcttgcatcaggagc ccaaatcttg tgacaaactt 840
 cacacatggc caccgtggccc agcacctgaa ctccgggggg gaccgtcaatg cttccttc 900
 cccccaacaa ccaaggacac cctcatgatc tccccggacc ctgaggtcac atpcgtgtgt 960
 gtggacgtqa gccacgaaga ccctgggggtc aagtccact gtacgtgg cgcgtggag 1020
 gtgcataatgt ccaagacaaa ggcgcggggag gaggactaca acagcacgtta ccgtgtggtc 1080
 agccgtctca ccgtcttcga ccaggactgg ctgaatggca aggaggataca gtgcagggtc 1140
 tccaaacaaag ccccttcggc ccccatecgag aaaacatctt ccaaggccaa aggccggcc 1200
 cgagaaaccac aggtgtacac cttgtggggatc tccggggatg agtgcaccaa gaacctggc 1260
 agcctggactt gcttgtcaaa aggcttcata cccagcgaca tcggcgtggaa gtggggagagc 1320
 aatgggcagc cggagaaaca ctacaagacc acggccccc tgcgtggactc cgcgggttc 1380
 ttcccttcctt acagacaaatg caccgtggac aagagcagg ggcggcgggg gaacctttc 1440
 tcatgtctcg tgatgtatca ggtctgtcac aaccactaca cgcagaagag ccttccttc 1500
 ttccgggtta aatgtatctga a 1521

<210> 240

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 240

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10			15			
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
				20				25				30			
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Va	Thr	Met	Thr	Cys	Arg	Ala	Ser
				35				40			45				
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
				50			55				60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	65				70					75					80
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90				95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
		100				105			105				110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Gly	Leu	Lys
	115				120					120		125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130				135					135		140			
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
	145					150				155					160
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
	165					170				170					175
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
	180					185				185			190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
	195					200				200			205		
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215				215			220		
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
	225					230				235					240
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
	245					250				250			255		
Gly	Thr	Gly	Thr	Val	Thr	Val	Ser	Ser	Asp	Gln	Glu	Pro	Lys	Ser	
	260					265				265			270		
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
	275					280				280			285		
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
	290					295				295			300		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
	305					310				315					320
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	325					330				330			335		
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	340					345				345			350		

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

```

<210> 241

5211> 1

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 241

ggatgtttt tgaaccttgtt cccatccggg gcccattactt taatctcagt aaatgaaatt 60
ttttgtatatt gctgcctgcac ctactgtttt gcccccaagat gcagagagag aaggaggaat 120
gagagatttgaa gaaggaaaag tgtacccctt gtataatcgt at 162

<210> 242

<211>

<212> PRT

<213> Artificial sequence

<220>
<221>

<223> Fusion polypeptide

4000 242
Ala ASP P

1 Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro
 5 10 15
 20 25 30
 Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val
 35 40 45
 Arg Pro Val
 50

<210> 243

<211> 399

<212> DNA

<213> APL111111 sequence

<220>
<223>

4229 Fusion polyimide

406 245
aagcttata

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 tggacgttgc gtggaggcac caagctggaa atcaaacgg 399

<210> 244
 <211> 131
 <212> PRT
 <213> Artificial sequence

<220>
 <223> fusion polypeptide

<400> 244
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
 20 25 30
 Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
 35 40 45
 Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
 50 55 60
 Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile ser Gly
 65 70 75 80
 Ile Pro Ser Arg Phe Ser Gly Ser Gly ser Asp Phe Thr Leu
 85 90 95
 Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
 100 105 110
 His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu
 115 120 125
 Ile Lys Arg
 130

<210> 245
 <211> 368
 <212> DNA
 <213> Artificial sequence

<220>
 <223> fusion polynucleotide

<400> 245
 cagatccagt tggtycaatt tggaccctgag ctgaaagaacg ctggagagac agtcaggatc 60
 tcctgcgaagg ctctcggtta tgccctcaca actactggaa tgcagtgggt gcaagagatg 120
 ccaggaaagg gtttgaaatgg gatggctgg attaaaacacc cactctggag tgccaaata 180
 tggtagaaacg ttcaaggagc gtttgccttc tctttggaaa cctctgccaa cactgcata 240
 ttacagataa gcaacctcaa agatggggac acggctacgt attttctgtt gagatccccgg 300
 aatggtaactt atggccctggc ctacttttgtt tacttggggcc aaggggacact ggtcactgtc 360
 tctgtatca

<210> 246
 <211> 121
 <212> PRT
 <213> Artificial sequence

<220>
 <223> fusion polypeptide

<400> 246
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Arg Ile Ser cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr
 20 25 30
 Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Ile Cys Arg Arg Leu
 35 40 45
 Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys 75 80
 Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
 65 70 75 85
 Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

<210> 247
<211> 812
<212> DNA
<213> Artificial Sequence

<220>

<210> 248
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

```

<400> 248
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
      5          10        15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
      20         25        30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
      35         40        45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
      50         55        60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
      65         70        75        80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Asp Phe Thr Leu
      85         90        95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
      100        105       110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu
      115        120       125
Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
      130        135       140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
      145        150       155       160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
      165        170       175
Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys
      180        185       190
Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
      195        200       205
Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr
      210        215       220
Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr
      225        230       235

```

DOI: 10.1007/s00339-007-0303-2

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
245 250 255
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
260 265

<210> 249
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<210> 250
<211> 135

<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 250
MΩ ACB D

Mel	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1									10						15
Val	Ile	Met	Ser	Arg	Gly	Val	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala
								20				25			30
Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala
							35				40		45		
Ser	Glu	Ser	Val	Glu	Tyr	Tyr	Val	Thr	Ser	Leu	Met	Gln	Trp	Tyr	Gln
							50				55		60		
Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Ile	Ser	Ala	Ala	Ser	Asn	
	65					70				75					80
Val	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
							85			90					95
Asp	Phe	Ser	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Asp	Ile	Ala	Met
							100			105					110
Tyr	Phe	Cys	Gln	Gln	Ser	Arg	Lys	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly
							115			120					125
Thr	Lys	Leu	Glu	Ile	Lys	Arg									
							130				135				

<210> 251

<211> 369

<212> DNA

<213> Artificial sequence

<223> fusi

4232 *Fuson polyimide*

400 291
caggtqcaq

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 65 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr 70 75 80
 Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met 85 90 95
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly 100 105 110
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly 115 120 125
 Ser Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly 130 135 140
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly 145 150 155 160
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly 165 170 175
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp 180 185 190
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser 195 200 205
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr 225 230 235 240
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr 245 250 255
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser 260 265 270

<210> 255

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 255

atggattttc aagtgcagat tttcagcttc ctgtctaattca gtgtcttcagt cataatgtcc 60
 agaggagtcc acatcccgat gacacagtct ccacatccac tgcgtcgtc tctggggaggc 120
 aaatgtccaca tcacttgcaa ggcaagccaa gacattaaga agtatataagg ttgttaccaa 180
 cacaaggctc gaaaaggccc caggctgtct atatattaca catctacatc acagccaggc 240
 atccccatcaa gggttcaatgg aagtgggtct gggagagatt attccctcag catcagaaac 300
 ctggagcttc agatatttc aactttatgg tgcacaaatgt atgataatct tcatttgac 360
 ttccgtctgg ggacaaatggt ggaataaaaa cgg 393

<210> 256

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 256

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser 20 25 30
 Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala 35 40 45
 Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr His Lys Pro Gly 50 55 60
 Lys Gly Pro Arg Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly 65 70 75 80
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu 85 90 95
 Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln 100 105 110
 Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu 115 120 125

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ile Lys Arg
 130

<210> 257
<211> 362
<212> DNA
<213> Artificial Sequence
<220>
<223> fusion polynucleotide
<400> 257
 gatgtacagc ttccaggagtc aggacattggc ctcgtgaaac cttctcagtc tctgtctc 60
 acttgcgttc tcactggcta ctccatcacc agttggtttc acgtggaaatc gatccgacag 120
 ttccggaa acaaacttggaa atggatggc acatatacgcc acgacggatc gaataacttc 180
 aaccatcttc tcataaatcg aatccatccatc acatcgatca catctaaatggc ccagttttc 240
 ctgaatgttgc gtctctgtac tactggggac acatgtatcatc attttctgttc aagggactac 300
 ggtagtagtcg gagctatggaa ctactggggat caaggaacct cagtaccgt ctccctgtat 360
 ca

<210> 258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 258
 Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
 20 25 30
 Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45
 Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
 50 55 60
 Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95
 Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Val Thr Val Ser Ser

<210> 259
<211> 806
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 259
 aagcttatgg attttcaagt gcagattttc agtttccgtc taatcgtgc ttccgtatcata 60
 atgtccagag gatgtccgat ccagatgaca cagttccatc cttccatgtc tgcatctcg 120
 ggggccaaag tcaccatcac ttgcggggca acggcaacaga tttaaaggatc tatgggttg 180
 taccacacaca aycctggaaa aggtccccgg cttgtccatcatc attaccatcata taccatcag 240
 ccaggccatc catcaagggt cttgtccatc ggggtctggaa gaggttttc cttccatgtc 300
 agaaaaacctgg agccgttggaa tattttcaact tattttatgtc aacagtatgtc taatccatc 360
 ttgtactggc gttccggggac aaaggatggaa ataaaaacgggg ttggccgttgg ctggccgttgg 420
 ggtgggttggg ttggccggcc atctgtatgtc cagttccatc agtccatgtc ttggccgttgg 480
 aaacccttcgc agtctctgtc ttccatgtc cttgtccatc gctactccat caccatgttgc 540
 ttctactggaa actggatgtcc acatgtttccg gggaaacaaac ttggaaatggat gggccacatata 600
 agccacacgcg gtaggaaataa ctacaacccca tctctcataa atcgtatc cttccatgtc 660
 gacacatcta agaaccaggat ttccctggaa ttgtatgttgc ttgtactgtc ggacacacgtc 720

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 acatatttctt gtgcgaagaca ctacggtagt agcggagcta tggactactg gggtaaaggaa 780
 acctcagtc cccgtccctc tgatca 806

<210> 260
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 260
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
 20 25 30
 Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
 35 40 45
 Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
 50 55 60
 Lys Gly Pro Arg Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
 65 70 75 80
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
 85 90 95
 Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
 100 105 110
 Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
 115 120 125
 Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Gly Ser Asp Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro
 145 150 155 160
 Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
 165 170 175
 Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
 180 185 190
 Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
 195 200 205
 Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
 210 215 220
 Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
 225 230 235 240
 Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
 245 250 255
 Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265

<210> 261
 <211> 417
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 261
 atggcatgga gctgcattat ttctttcttg gtatcgtaa ttacagggtgt ccattcccg 60
 gtcgaactgc agcagtccgg ttctgaacta gggaaacctg gggcctcgat gaactgtcc 120
 tgcgaactgt caggctacat attcacagat cactatattt ctgggtgaa acagaadgct 180
 ggagaaaaggcc tgcagtgtat agggaaatgtt tatggatggaa atgggtgtac aagcttcaat 240
 caaaaaatccg aggcccaaggc tcacaggatct gtatgtaaaa tctctagcac agccatcac 300
 gaactcgcga gcctgcacatc caggatgtt gcccatttactt acttgtcaag aaggccggta 360
 gcgacgggcc atgcataatggaa ctactgggtt caggggatcc aagttaccgt ctccctca 417

<210> 262
 <211> 139
 <212> PRT
 <213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 262

Met Ala Trp Ser Cys Ile Ile Phe Phe Leu Val Ser Val Ile Thr Gly
1 5 10 15
Val His Ser Gln Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys
20 25 30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
35 40 45
Thr Asp His Tyr Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu
50 55 60
Gln Trp Ile Gly Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn
65 70 75 80
Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser
85 90 95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile
100 105 110
Tyr Tyr Cys Ala Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr
115 120 125
Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
130 135

<210> 263

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 263

atgttgtata catctcgact cttgggctt ttactctct ggatttcagc ctccagaatg 60
gacatagtgc tgacttcgacat ccggccactt ctgtctctaa ttccggaga aaagtccaca 120
atgaccgtga aqaccgtca gaatattggc acaatcttac actggatatac cccaaaacaa 180
aaggagggttca caagggttct catcaatgt gcttcgcagt ccattccgg gatccccccc 240
agatttcgtg ccaatgggttc gggaaacatgt ttcaatccca gcatcaatad ccttggaggtct 300
gatgtatctcg gaattttata ctgtcaacaa aatgtaaatgtt ggccgttcac gttcgttct 360
ggccaacaaatggagataaa a 381

<210> 264

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 264

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
1 5 10 15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
20 25 30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
35 40 45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
50 55 60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
85 90 95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100 105 110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
115 120 125

DOI: 10.1007/s00339-007-0303-2

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07-24-03.txt

<210> 265

<211>

<212> DNA

1220

<220>
<223> fusion polynucleotide

<400> 265

aaggcttagg	attttcaactg	gcagattttc	agtttcgtc	taattcagtgc	ttcagtcata	60
atgtcccgag	gagtgcacat	tgttcgtact	catgtcccg	ccaccatgcg	ttgttgactca	
ggatagatgc	tcttcgttcc	ctggcaggccc	aggccagata	ttagcacta	tttacatccgg	180
tatccaacaa	aatcgtatcg	gttcccaagg	ttttccatca	aatatgttc	ccatccatcc	
tctggatgttc	ccttcggatgt	cgttgcgatc	ggatccagggt	cattatgttc	tttcgtatcc	240
aacatgttgtt	aaacctgtaga	gttggatattt	atttatgttc	aaatgttcac	cagttatcc	
tggatgttcg	gttggggggcc	caatccgttt	atccatgggg	aaatgttcgtc	aaatgttcgtc	300
ggttgtttcg	gttgggggggg	atccatgcate	catgtttgg	ttttccatcc	cagttatcc	
aaggcttggag	aaacatgtttt	aaacatgtttt	aaatgttcgtc	ttttccatcc	cagttatcc	360
ggaaatgtcgt	ggatgtccaa	aaatatgttgc	aaatgttcgtc	ttttccatcc	cagttatcc	
aaaaacccatct	ggatgtccaa	aaatattatgt	aaatgttcgtc	ttttccatcc	cagttatcc	420
gaaacccatctg	caacaatctgc	attttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
acgtatgtttt	gtgttgcatac	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	480
ggccaaaggaa	cgttgcatac	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
acatccatccc	cgttgcatac	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	540
caaaaatccat	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	600
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	660
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	720
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	780
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	840
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	900
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	960
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1020
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1080
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1140
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1200
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1260
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1320
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1380
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1440
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1500
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1560
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1620
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	
ggatgtttttt	ggatgtttttt	ttttatgtac	aaatgttcgtc	ttttccatcc	cagttatcc	1677

<210> 266

<210> 200
<211> 552

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 266

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
      5          10          15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
      20          25          30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
      35          40          45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
      50          55          60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
      65          70          75          80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
      85          90          95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
      100         105         110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
      115         120         125
Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
      130         135         140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
      145         150         155         160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
      165         170         175

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys
 180 185 190
 Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
 195 200 205
 Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Gln Thr Ser Ala Asn Thr
 210 215 220
 Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr
 225 230 235 240
 Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
 245 250 255
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asp Leu Glu Pro Lys
 260 265 270
 Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu
 275 280 285
 Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 290 295 300
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 305 310 315 320
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 325 330 335
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 340 345 350
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 355 360 365
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 370 375 380
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 385 390 395 400
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 405 410 415
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 420 425 430
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 435 440 445
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 450 455 460
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 465 470 475 480
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 485 490 495
 Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala
 500 505 510
 Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr
 515 520 525
 Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu
 530 535 540
 Arg Arg Glu Ser Val Arg Pro Val
 545 550

<210> 267

<211> 1683

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 267

```
aagcttatgg atttcaagt gcagatttc acgttccatgc taatcagtgc ttcaagtccata 60
atgtccaggag gagtcgacat tggcttacc caaatcccg ctctttggc tggcttcta 120
ggtcaggag ccaccatctc ctgcagacc agtggaaatgt ttgaatatta tggcacaatgt 180
ttaaatcgat ggttacaaaca gaaacccaga cagcccccca aactccatcat ctctctgc 240
ttcaatcgat aatctgggggt ccctgcggc tttatggccca gtgggtctgg gacaaatctc 300
agccctaaaca cccatcgatgttggaggat gatattggca tgatattctgc tcagccaaatgt 360
aggaaatggct ctggacatgttggggatcc accaaatgttggcccaatccaaacgg gggttgcggcgt 420
ggcttcggccggc ggggttgcggcc ggttgcggcc ggttgcggcc ggttgcggcc 480
cctggccctgg tggccgcctc acagagccctg tggccgcctc acagagccctg gacccgtctc 540
ttaaatccggat atggtgtaaa ctgggttccgc cagccttcgc gaaagggttccgc 600
```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ggaatgatgggggtatgg aagcacagac tataatttcg ctcttcaaatc cagactgagc 660
 atcaccaaagg acaactccaa gagccaaatgt ttctttaaaaa tgaaacgttc gcaacttg 720
 gacacagccaa gatactactgt tgccagatgt gtttatagtta acttttcattt cttatgttatg 780
 gactactgtgg gtcaaggaaatc ttccatgttccacg ttcttcctcag atctggagcc caaafttttc 840
 gacaaaactt acacatcccc accgcgtccca gaccccttgcac ttcttgggggg atcgctcgtc 900
 ttcccttcctt ccccaaaaccc caaggacacc ttcatgttcc cccggacccc tgagggtcaca 960
 tgcgtgggtgg tggacgtgtgg ccacggacacc ttcatgttcc cccggacccc tgagggtcaca 1020
 ggcgtggagg tggatataatgc caagacaaatgg ccgcgggggg agcgttacaa cagcacgtac 1080
 cgtgtggtcg gcttcctcactc cgttcctcactc caggactgtgc taaatggcaaa ggatgtacaa 1140
 tgcacgggtctt ccaaaacaaaccc cttcccaaccc cccatcgaga aaacccatctc caaaatccaa 1200
 gggcagccccca gagaacccca ggtotatcacc ctgcctccat cccgggtatgca gctgactaa 1260
 aaccagggtca gctgttccatc cttccatcacc ttcatgttcc cccggacccc tgagggtcaca 1320
 tggggagagca atggggcagcc ggagaacaccatc tacaagggaccc ccgcgttccgt gctgttccatc 1380
 gacgttcccttca cttccatgttccgt gatgttccatc accgttccatc aagggatgttccgt gacgttccatc 1440
 aacgttcccttca cttccatgttccgt gatgttccatc accgttccatc aagggatgttccgt gacgttccatc 1500
 cttccatgttccatc accgttccatc aagggatgttccatc tccatgttccatc ggcatttacc 1560
 ttaatctcgttccatgttccatc accgttccatc tccatgttccatc ggcatttacc 1620
 tgcagagaga gaaaggaggaa tgagatgttccatc accgttccatc aagggatgttccatc 1680
 gat 1683

<210> 268

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 268

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
 20 25 30
 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
 35 40 45
 Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
 50 55 60
 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn
 65 70 75 80
 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
 85 90 95
 Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met
 100 105 110
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly
 115 120 125
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly
 145 150 155 160
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
 165 170 175
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly
 180 185 190
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp
 195 200 205
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser
 210 215 220
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
 225 230 235 240
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr
 245 250 255
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 385 390 395 400
 Pro Arg Glu Pro Glu Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
 500 505 510
 Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
 515 520 525
 Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
 530 535 540
 Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 545 550 555

<210> 269

<211> 1665

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 269

aagtccatgg atttcaagt gcagatttc acgttccgtc taatcgtgt ttcaagtatca 60
 agtccatgg gagtcgcacat ccaggatgaca cagtcgtccat cttcacatcg tgactctcg 120
 ggaggccaaag tcaccatcac ttgcaggcga acggcaacaa tttaaqaagta tataatgttg 180
 taccacaaac agcttgcggaa aggtccccagg ctgtctatcat attacacatc tacattacag 240
 ccaggatccat catcaagggt ctatggaaat gggctctggat gagatttttc cttcagatc 300
 agaaaaacctgg agcttcggaaa tatggcaact tattatgtgtc aacggatgtaa taatcttcca 360
 ttatggatccggc gtgcggggc aaatgggtaa aaaaaacggg gtgcgtgtgg ctccggcggt 420
 ggtgggttcgg gtgcggccgg atctgtatca cagtcgtccat cttcgtccat cttccgttg 480
 aaaccttccatc agtcttcgtc tcttcacatcg tctgtctatcg gttactccat caccgttgt 540
 ttctactgtt agtggatccg acatgtttccg gggaaacaaac tggaaatggat ggccacatata 600
 agccacatcg tgatggaaata ctacaaacccca tcttcataatc atcgaatctc catcactcg 660
 gacacatctt caaaatccgtt ttcttcgtaa tgatgttctg tgatgtactgc ggacacatcg 720
 acatatttttctt tgcaaaatcgca acggcgatgtt acggcgatgtt tggtactactg gggtcaaggaa 780
 accttcgttca cctgttccctc tgatgttgcgaa acatccatctt ctgacaaatcg tccacatctt 840
 ccacgggtccc cagcaatcgta acatcttgggg ggatgtcgatc ttttccttcc ccccccacaa 900
 cccaaaggacca cccatcgat ctcccgaccc cttcgaggatc catcggtgtt gttggacgttg 960
 agccacacaaag acccttgcgggt caaattttcaac ttgttacgtgg accggcggtgg ggttcataata 1020
 gccaacaaatcg agccggccggg ggaaatcgatc aacatcgatcg accgtgtgtt cagcgttc 1080
 agccatggatcc accaggatgtt gtcgtatggc aaggatgtca atgtccaaatcg ctccaaatcg 1140
 gcccctccatcg ccccccattcg gaaaacccatc ttccaaatcgca aaggggcaggcc cccggaaacca 1200
 Cagggttgcata cccctggccctt atccgggtatc ggcgttgcacca aqaaacccatcg caggctcgat 1260
 tgcttgcataa aagggttcttca cttccatcgatc atcccggttg atgtggatggg caatggcgatc 1320
 Cggggaaatcg actacaaatcgca cagccgttcc acggcgatgtt acggcggttc ctttccttcc 1380
 tacagcaacgg tcaccgttgcgaa caaaggatcgatc tggcggcagg gggacgtgtt ctatcgatcg 1440
 gtgtatgttgcgatc aggtctctgcgaa cccacatcgatc acggcgatgtt acggcggttc ctttccttcc 1500
 aaatcgatgttgcata cttccatcgatc tggggccatcgaa cttaaatcgatc agttaaatcgatc 1560
 atttttttgttgcata cttccatcgatc ttttgcggccatcgaa gatgtcgatgtt gggacgtgtt gggacgtgtt 1620
 aatcgatgttgcata cttccatcgatc tggggccatcgaa gatgtcgatgtt gggacgtgtt gggacgtgtt 1665

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 270
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 270

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asn Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gln Leu Val Lys Pro
145 150 155 160
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
165 170 175
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
180 185 190
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
195 200 205
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
210 215 220
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
225 230 235 240
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
245 250 255
Gln Gly Thr Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

2011-01-01

WO 2005/037989

PCT/US2003/024918

```

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
  470          475          480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
  485          490          495
Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr
  500          505          510
Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys
  515          520          525
Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg
  530          535          540
Glu Ser Val Arg Pro Val
  545          550

```

<210> 271
<211> 1653
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<210> 272
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

```

<400> 272
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
      1           5           10          15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
      20          25          30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
      35          40          45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
      50          55          60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
65 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn 70 75 80
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg 85 90 95
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg 100 105 110
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly 115 120 125
Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser 130 135 140
Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr 145 150 155 160
Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly 165 170 175
Asn Val Tyr Gly Gly Asn Gly Tyr Ser Tyr Asn Gln Lys Phe Gln 180 185 190 195
Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met 200 205 210 215 220
Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala 225 230 235 240
Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly 245 250 255
Ile Gln Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys 260 265 270
Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser 275 280 285
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 290 295 300
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp 305 310 315 320
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn 325 330 335
Ala Lys Thr Lys Pro Arg Glu Gln Gln Tyr Asn Ser Thr Tyr Arg Val 340 345 350
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 355 360 365
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys 370 375 380
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 385 390 395 400
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr 405 410 415
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 420 425 430 435
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 440 445 450
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 455 460
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu 465 470 475 480
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly 485 490 495
Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile 500 505 510
Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala 515 520 525
Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser 530 535 540
Val Arg Pro Val 545

<210> 273

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

Int. J. Environ. Res. Public Health 2021, 18, 1021

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> fusion polynucleotide

<210> 274

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 274
Mat. & Engg.

Met Asp Phe Gin Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile val 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45 50
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235

WO 2005/037989

PCT/US2003/024918

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 275

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligo to make IgG hinge SSC mutant using IgG hinge
SSS as a template

<400> 275

gttggttgatc aggagccaa atcttctgac aaaactcaca catctccacc gtggccagca 60
cctg 64

<210> 276

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligo to make IgG hinge SCS mutant using IgG hinge
SSS as a template

<400> 276

gttggttgatc aggagccaa atcttctgac aaaactcaca catgccacc g 51

<210> 277

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligo to make IgG hinge CSS mutant using IgG hinge
SSS as a template

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 seq List Text 07.24.03.txt

<400> 277
gttggatcaggagccaaatcttgatc aaactcac
39
<210> 278
<211> 52
<212> DNA
<213> Artificial sequence

<220>
<223> 3' oligo to amplify constant regions for creating IgG hinge mutants

<400> 278
gttggttctatcattttac ccggagacag ggagaggctt ttctgcgtgt ag
52
<210> 279
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligo that mutates VH1 L to S

<400> 279
ggagggtggaa gcttcaggc ttatctacag cagtctgggg ctgagtcgggt gaggcc
56
<210> 280
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for amplifying IgG1 constant regions

<400> 280
gtctcttagac tacatattac ccggagacag
30
<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for first PCR to insert IgA hinge into IgG1 CH2-CH3

<400> 281
ccatctccatcaactccacc taccatctccatcg caccgtaaact cctg
54
<210> 282
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> 5' oligo for second PCR to insert IgA hinge into fused to IgG1 CH2

<400> 282
gttggatcaggatgttcc ctcaactcca cttccccat cttcccaact
50
<210> 283
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<400> 283

```

aagtccggc ccatggattt tcaagtgcg attttcagct tcctgtcta cagtgcttc 60
gtcataatgg ccaggaggaca aatgttgcctt tcccaagtcc cagaacatctt gtctgcattc 120
ccaggggaga aaggtcacaat gacttgcaga gccagctcaa gtgtaaaggta catgactgg 180
taccaggcaga agccaggatc ctccccccaaa ccttggattt atgccccttc caacctggct 240
tctggagttc ctgttcgttt ctagtgcgtt gggttctggga ccctttactc ttccacaatc 300
aagcagatgg aaggctgaaaga tgctgcactt tttacttgcg aagcagtgaggg ttttaaccc 360
cccacgttgc tgctggac caagctggag ctgaaaggatg gcgggtggctc gggcggtgt 420
ggatctggag gaggttggag ctctcaggct tatctacagc agtctgggc tqagctggp 480
aggctctgggg ctctcaggatg aaggttttcg gttcacattt taccatgtc 540
aatatgcact gggtttaaaggc gacaccatgaa cagggccctgg aatgtgatgg agtcatttat 600
ccaggaggatg gttagatcttc ctacatcgatc aagtttcaggg gcaaggccac actgtgtt 660
gacaatctt ccacgcacgc ctacatgcgc cttagcaggcc tgacatcttga agactctcg 720
gtctatcttc gtgcagaatgg ggtgtactat aatgtatctt ctgtgttctt ctagtgcgtt 780
ggcacaaggaa ccacgcacgc ctgttcgtat ctagcaggctt ctcaacttcc accatcccc 840
tctccctcaaa ctccatccatc cccatcttcc ttatgttccctt tggtttccctt gggggggaccg 900
tcagtcatttc ttttcccccc aaaaaaccatgg aacaccctca tgatctccctt gaccctctgg 960
gtcataatggcc tggtgttgcg ctgtggccatc ggaaaggccctg aggttcaggat cttttttttt 1020
ttggacccgc tggtggatgc taatgtccaa acaaaggccgc gggaggagac tgacaaacagg 1080
acgttccggc tggtttccatc ctccatccatc ctgtggccatc ctgtggccatc tggtttccatc 1140
taacatgtca aaggcttccaa caaaaggccgc ctacatccatc tggtttccatc tggtttccatc 1200
gccaaaggccgc acccccgaga accacatggt tgacccatccgc ccccatcccg ggatgtatgt 1260
accacaaaggccgc acccccgaga accacatggt tgacccatccgc ccccatcccg ggatgtatgt 1320
gttggatgtggg aaggtaatggc tgatgtttttt cccttcatcgtt aagtttcaggc tggtttccatc 1380
gatccatggatggt gttttttttt cccttcatcgtt aagtttcaggc tggtttccatc tggtttccatc 1440
caggggaaacgc tttttttttt cccttcatcgtt aagtttcaggc tggtttccatc tggtttccatc 1500
aaggcccttc ccctgttctt gggtaatgtatc tgtagt 1536

```

<210> 284

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 284

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser 1
5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile 20
25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser 35
40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser 50
55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro 65
70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile 85
90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp 100
105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys 115
120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser 130
135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala 145
150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gln Tyr Thr Phe Thr Ser Tyr 165
170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile 180
185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe 195
200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr 210
215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys 225
230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr
 260 265 270
 Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350 355
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 385 390 395 400
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gln Pro Glu Asn Asn
 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 285

<211> 1584

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 285

```
aagtggccg ccatggatt tcaagtgcag atttcagct tcctgtaat cagtgctta 60
gtcataattt ccagggaca aattgttc tccccagtc cagaatcc tgcgcattct 120
ccaggggaga aggtcacaat gacttgcagg gcccgcctaa gtgtaaatgtt catgcactgg 180
taccaggaga agccaggatc ctcccccaat cctcgattt atgcggccatc caacctggct 240
tcctggatcc ctgtcgctt ctgtggcagg ggttgcggg ccfttttac tctccacata 300
agcagatgg aggtcgaaat tgctggccatc tttacttgc agcagtggag tttaaccctt 360
ccccacgttgc gtgtggggcc caaagtgggg ctggaaatggt gggttgccggc gggcggttgt 420
ggatctgggg cttcgtggat ctgcggatc ttatctacgc agtctggggc tgagctgggt 480
aggcgttggg cttcgtggatc gtatgttgcg aaggcttgcg gtcacacattt taccatgtac 540
aatatgcact gggtaaaatc gacacttgcg caggccgttgc aatggatgtgg agctatattat 600
ccaggaaatgt gtgtatcttc ctacaaatcg aagttcacgg gcaaggccac actgtatgtt 660
gacaaatctt ccacacatgc ctacatgcg ctccagcgtc tgacatcttg agactctggc 720
gtctatitctt gtgcgaatgtt ggttgcattt agtaacttctt actgttactt ctgtgttgg 780
ggcacaggga ccacgggttcac gtttgcgttccatc gatcggccatc ttccctcaat tccacactacc 840
ccatctccctt caacccccc taccctccatc cctctatgtt gccaacccccc actgtacty 900
caccgacccgg ccctcgaggaa ctgcgttccatc ggtgttgcggg gtcatccatc gtgcacacty 960
accggccgttgc gagatgttgc aggtgttccatc ttccatgttgc cccctccatc tgggaaagagc 1020
gtctgttgcgaa gaccatcttc ctgggttgcgttgc acatgttgcg cttgcacatc tgcttccccc 1080
ccggggctgtg ccggccatgc gaaatcttgc agaacatcttc ttccatgttgc cttgcacatc tgcttccccc 1140
gatcccaagaatcc cccggccatc tcääaaatccg gaaacacatc ccggccggac 1200
gtccacactgc ttggccggcc gtcggaggat ctggccgttgc acgagctgtt gacgtctggc 1260
tgccctggcacttgc ttggccggcc gtcggaggat ctggccgttgc acgagctgtt gacgtctggc 1320
gactgtggcccc gtcggaggat ctggccgttgc acgagctgtt gacgtctggc 1380
accacccatgc ttggccggcc gtcggaggat ctggccgttgc acgagctgtt gacgtctggc 1440
accttctcttgc gatccatgc ttggccggcc gtcggaggat ctggccgttgc acgagctgtt gacgtctggc 1500
```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gaccgcgtgg cgggtaaacc caccatgtc aatgtgtctg ttgtcatggc ggagggtggac 1560
ggcacctgtc atgtataatc taga 1584

<210> 286
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 286
Met Asp Phe Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Gly Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445
Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 450 455 460
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met
 500 505 510
 Ala Glu Val Asp Gly Thr Cys Tyr
 515 520

<210> 287
<211> 775
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 287
 tgatcaggcca gtttccctcaa ctccacccat cccatctccc tcaactccac ctaccccatc 60
 tccttcatcg tgccacccccc gactgtcact gcaccgcacg gccttcgagg acctgtctt 120
 aggttcggaa gcgatctca cctgtcacact gacggggccctg agagatccct cagggtgtcac 180
 cttcacctgg acggccctcaa gtgggaagag cgtgttcaa ggacccatcg acctgtgacct 240
 ctgttgctgc tacagcgctgt ccagtgttgc gccgggtctgt gcccggccat ggacccatcg 300
 gaagacatttc acttgcactg ctgcctfacc cggatccaaq accccgttaa ctggcacttc 360
 ctcaaaaatcc ggaaacacat tccggcccgaa ggttccatcg ctggccggc cgctggaggaa 420
 gctgtggccctt aacggactgg tgacgtgtac gtgtccttgca cgtagcttca gccccaaaggaa 480
 tggatcgatcg ctgttgctgc agggggtcaca ggagctgccc cgccgagaatg acctgtacttg 540
 ggcatccccgg caggaggccca gcaaggccatc gctgtgacca gcatactcg 600
 ctgttgccggc gggactgtgg aagaaggggggg taccttttc tgcatgggtt gccacggaggc 660
 cctggccgtcg gcttcacatc agaaagaccat cgaccgcgtt ggggttaaac ccaccatgt 720
 caatgtgtctt gttgtatcg gggagggtgg cggcacccatcg tactgtataat cttaga 775

<210> 288
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 288
 Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15
 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20 25 30
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35 40 45
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50 55 60
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65 70 75 80
 Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85 90 95
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
 100 105 110
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
 115 120 125
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
 130 135 140
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 145 150 155 160
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 165 170 175
 Tyr Leu Thr Trp Ala Ser Arg Gln Gly Pro Ser Gln Gly Thr Thr Thr
 180 185 190
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 195 200 205

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List.Text 07.24.03.txt
 Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
 210 215 220
 Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
 225 230 235 240
 Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
 245 250

<210> 289

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR IgA hinge-CH2 CH3

<400> 289

gttggtttcia gattatcagt agcagggtgcc gtccacatcc gccatgacaa c

51

<210> 290

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 290

agatctcaag aagatgaaag gattgttctt gttgacaaca aatgttaagtg tgcccggtt 60
 acttccaggaa tcatccgttc ttccggaaat cctaatacgagg acatgttgga gagaaacatc 120
 cgaattttat ttcctctgaa caacaggaaat aatatctcttg atccccactc accatgttggaa 180
 accaggattt tgatccatctt gttgtaccc agctgtaaaa aatgtgtatcc tacagaaatgtt 240
 gagctgttata attcgtatgt tactgttacc cagagaaata tcttgtatgtt agacagtgtt 300
 acagagactt gttacactta tgacagaaac aagtgttaca cagctgttgtt cccacactgtt 360
 tatgtgttgtt agacacaaat ggtggaaaca gccttaaccc cagatgttccgtt ctatcctgtac 420
 taatctttaga 429

<210> 291

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 291

Arg Ser Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys
 1 5 10 15
 Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn
 20 25 30
 Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn
 35 40 45
 Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val
 50 55 60
 Tyr His Leu Ser Asp Leu Ser Cys Lys Lys Cys Asp Pro Thr Glu Val
 65 70 75 80
 Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp
 85 90 95
 Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys
 100 105 110
 Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val
 115 120 125
 Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro
 130 135

<210> 292

<211> 36

<212> DNA

DOI: 10.1007/s00339-007-0301-2

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Artificial Sequence

<220>
<223> 5' oligo to PCR J chain

<400> 292
gttgttagat ctcaagaaga taaaaaggatt gttctt

36

<210> 293
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to PCR J chain

<400> 293
gttggttctta gatttagtcag gatagcaggc atctgg

36

<210> 294
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> 4 carboxy terminal amino acids deleted from IgA₂

<400> 294
Gly Thr Cys Tyr
1

<210> 295
<211> 763

~~100~~ <212> DNA

<213> Art

www.ijerpi.org | 10

<223> fusion polynucleotide

£400 > 293

<210> 296

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400>_296

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15
 Pro Thr Pro Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20 25 30

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35 40 45
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly val Thr Phe Thr Trp Thr
 50 55 60
 Pro Ser Ser Gly Lys Ser Ala val Gln Gly Pro Pro Asp Arg Asp Leu
 65 70 75 80
 Cys Gly Cys Tyr Ser Val Ser Ser val Leu Pro Gly Cys Ala Glu Pro
 85 90 95
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
 100 105 110
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
 115 120 125
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
 130 135 140
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 145 150 155 160
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 165 170 175
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
 180 185 190
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 195 200 205
 Gly Asp Thr Phe Ser cys Met Val Gly His Glu Ala Leu Pro Leu Ala
 210 215 220
 Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
 225 230 235 240
 Asn Val Ser Val Val Met Ala Glu Val Asp
 245 250

<210> 297

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for construct with 4 amino acid deletion
in IgA CH3

<400> 297

gttggttctta gattatcagt ccaccccgcc catgacaaca gacac

45

<210> 298

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 298

aagcttgcgc ccatggatt tcaagtgcag attttcagct tcctgtcaat cagtgcttca 60
 gtcatataat ccaggagaca aatttgttcc tccccacttc cagaatctt ctgtgcattc 120
 ccaggggaga aaggccaaat gacttgcagg gccagtcataa gtgttaagttt catgcactgg 180
 taccaggcaga aqccaggatc ctccccaaa cccgttggattt atgccccatc caacctgg 240
 tctggaggcc ctgtctgtt cagtggcagt gggtttggga ctcttttactt ttccacatc 300
 agcagagttt aggctgaaga tgctgcactt tattactgcc agcagtggag tttaacccta 360
 cccacgttcc gtgtctggac caagctggag ctgaaaaggatg gcccgtggctt gggccgtgtt 420
 ggatctggag gaggttggag ctcttcaggcc tattctttagc agttctgggc tgactgttg 480
 aggcttgggg ctctcgttggat gatgttgcggc aaggcttgcggc gctcacatcatc taccaggatc 540
 aatatgcactt ggtttaaaaggc gacacttgcg caggccctgg aatggattttt agttttttt 600
 ccaggaaatgg ttgtatacttc ctatcaatcag aatgttcaagg qcaaaaggccac actgtttttt 660
 ccacaaatccctt ccacgcacgc cttatcatcg ctcaatcgcc cttcaggccqcc tgacatcttc 720
 gtcttattttt gtgtcaaggat ggtgttactat agtaacttctt atctgttactt ctgttgcgttgg 780
 ggacacggaa ccacggccac cttccatcttc cttccatcttc gttccctcaac tccacccatc 840
 ccatctccctt caacttcaccc taccctccatctt cttccatcttc gttccctcaac tccacccatc 900
 caccggccggccatc cttccatcttc gttccatcttc gttccatcttc gttccatcttc gttccatcttc 960
 accggcccttgg aagatgttgcacc aggtgttgcacc ttccatcttc gttccctcaag tggaaagagc 1020
 gttccatcttc gttccatcttc gttccatcttc gttccatcttc gttccatcttc gttccatcttc 1080

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

ccgggtgtc cggagccatg gaaccatgg aagaccttc ctggactgc tgccctaccc 1140
gagtccaaag ccccgcttaac cgccccctc tcaaattcg gaacacatt ccggcccgag 1200
gtccacccgc tgccggccg gtcggaggag ctggccctqa acgagctgtg caccgtqacg 1260
tgccctggcac gtggctttag ccccaaggat gtggctggc gtggctgtca gggttcacag 1320
gagctggccc gcgagaagta cctgacttgg gcattcccgc aggagccgg ccagggcacc 1380
accacccttcg ctgtgaccac catactgcgc gtggcagccg aggactggaa gaaggggac 1440
accctttctc gcatgttggg ccacgggcc ctggccgtgg cttcacaca gaagaccata 1500
gaccgcttgg cgggtaaacc cacccatgtc aatgtgtctg ttgtcatggc ggaggtggac 1560
tgataatcta ga 1572

```

<210> 299

<211> 516

<212> PRT

<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 299

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
 405 410 415
 Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
 420 425 430
 Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
 435 440 445
 Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile
 450 455 460
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met
 500 505 510
 Ala Glu Val Asp

515

<210> 300

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 14 amino acids deleted from IgAH-T4 (so that total
of 18 amino acids deleted from wild type IgA CH3)

<400> 300

Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
 1 5 10

<210> 301

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for engineering 14 amino acid from IgA-T4

<400> 301

gttgcattca gattatcatt taccggccaa cgccgtcgatg gtctt

45

<210> 302

<211> 709

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 302

tgatcagccaa gttccctcaa ctccccatcac cccatctccc tcaactccac ctaccccatc 60
 iccccttcatgc tgccaaaaaaa gactgtcaat gcacccgaccg gcccctcgagg acctgtcttt 120
 aggttcagaa ggcatccatca cgtgcacact gaccggccctg agagatgcct cagggtgtcac 180
 ctttacccctgg acgtctttaa gtggggadag gtgtgttcaat ggaccacctg accgtgaccc 240
 ctgtgtgttc tacagcgtgt ctggatgtcc gccgggtgt gccgagccat ggaaccatgg 300
 gaagacccctt acttgcactg ctgcctacc ctagtccaag accccggctaa ccgcacccct 360
 ctccaaaatcc gaaaacacat tcggcccca ggtgcacccctt ctgcggccgc cgtggaggaa 420
 gttgtggccctt aacgcgtctg tgacgtctcc ggtgccttgcga ctgtggcttcc gcccccaaggaa 480
 ggcacccccc cggaggccca gccggggccac caccacccctt ctgttgacca gcatactcgcc 600
 ctgtggcaccg gaggacttgg aaaggggggaa cacccttcc tgcattgttgg gccacggaggc 660
 cctgtccgttg gccttccatcac agaagacat ccacccgttg gccgggtaaa 709

<210> 303

<211> 236

<212> PRT

<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 303

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr PRO
 1 5 10 15
 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20 25 30
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35 40 45
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50 55 60
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65 70 75 80
 Cys Gly cys Tyr Ser Val ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85 90 95
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
 100 105 110
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
 115 120 125
 Pro Glu Val His Leu Leu Pro Pro Ser Glu Glu Leu Ala Leu Asn
 130 135 140
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 145 150 155 160
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 165 170 175
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr
 180 185 190
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 195 200 205
 Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
 210 215 220
 Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
 225 230 235

<210> 304

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 304

aagtccgtccg ccatggattt tcaagtgcag attttcagct tcctgtaat cagtgttcca 60
 gtcatataattt ccagaggaca aatttgttctc tccccagttc cagcaatccct gtcgtcatct 120
 ccaggggatc aggtcacatc gacttgcaag ggccagttcaaa ggttaaagtta catgcactgg 180
 taccacaga aagccaggatc ctccccccaa ccttggattt atggcccccattt caaccttgg 240
 tctggatctc ctgtctccctt ctaigtgcgtt ggttctggaa cttttttactc ttccacaaa 300
 agcagatgg aggtcgaa tgcgtccact tattactgc acgactggag tittaacccca 360
 cccacqttcg gtgtctggac caagcggggat tgaaagatg ggccgtgcgc gggcgtgtgt 420
 ggatcttggag gagttggggat ctctcggact tattcttacgc agtttggggc tgagttgg 480
 aggcttgggg cttctgtgaa gatgtcgttca agggcttctg gtcacacattt tacacgttac 540
 aatatgcattt gggttaaaggc gacactttaga cagggttggaa aatggatgg agtttattat 600
 ccaggaaatgtt gtgtataattt ctacaatctc aagtgttcaagg gcaaggccca actgttgc 660
 gacaatattcc ttccagcacatc ctatcatgcgtt ctccagcggcc tgacatctgc agactctgc 720
 gtcttattttt gtgtcaagatgtt ggttggatattt aatgttactttt atctggatctt ctatgttgcgg 780
 ggccatccaggaa ccacgtgttc ctgtttttttt gatcggccatgg ttcccttcaac ttccacatacc 840
 ccatcccttcc caacttccaccatc tccccatctt cttccatgtt gccaccccccc acgttctactg 900
 caccggaccggg cccctggggat gtttgcgttcaaa gatgttccatc gtgcacactgt 960
 accggcccttgc gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa 1020
 gtcgtttcaagg gacccatcttgc cccgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa 1080
 Cccggcccttgc ccggccatgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa 1140
 gagttttttttt gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa 1200
 gttccacccatc tggccgtccccc gttccacccatc tggccgtccccc gttccacccatc tggccgtccccc 1260
 tgccgtccccc gttccacccatc tggccgtccccc gttccacccatc tggccgtccccc gttccacccatc tggccgtccccc 1320
 gagttttttttt gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa gatgttgcgttcaaa 1380

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
accacccctcg ctgtgaccag catactgcgc gtggcagccg aggactggaa gaaggggcac 1440
acccttcctc gcatgttggg ccacgaggcc ctggcgctgg cttcacaca gaagaccatc 1500
gaccgcttgg cggtaaa 1518

<210> 305
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 305
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Ser Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Gly Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

```

 49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile
 450          455          460
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465          470          475          480
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485          490          495
Asp Arg Leu Ala Gly Lys
 500

```

<210> 306

<211> 924

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 306
962265†262

<210> 307

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 307

```

Met Gly Val Leu Leu Thr Gin Arg Thr Leu Leu Ser Leu Val Leu Ala
      5          10        15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
      20         25        30
Ala Val val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
      35         40        45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
      50         55        60
Gln Ala Asp Ser Gln val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
      65         70        75        80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
      85         90        95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gin Gly Leu Arg Ala Met Asp
      100        105        110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
      115        120        125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
      130        135        140
Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Cys Asp Lys Thr His Thr
      145        150        155        160
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
      165        170        175
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
      180        185        190

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 195 200 205
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 210 215 220
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 225 230 235 240
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 245 250 255
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 260 265 270
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 275 280 285
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 290 295 300
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 305 310 315 320
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 325 330 335
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 340 345 350
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 355 360 365
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 308

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 308

atgggggtac tgctcacaca gaggacgctg ctcagttctgg tccttgcaact cctgtttcca 60
 agcatggcga gcatggcaat gcacgtggcc cagcctgcgt tggtactggc cagcagccga 120
 ggcatcgccca gcttggtggtg tgatgtgc ttcggcggca aaggccatgtg gggtccgggtg 180
 acagtgccttc ggcaggctga cagccagggtc actgaatgtt gtgcggcaac ctatcatgtg 240
 gggaaatgtg tgacccttcct agatgttcc actgtcacgg gcacccatccag tggaaatcaa 300
 gtgaaacctta cttatccaaaatggggcc atactatccgt gycataggca gacttatacg tggcaagggtg 360
 gagttcatgtt accccacggcc atactatccgt gycataggca acggaaaccca gatttatgtt 420
 attgatccatgtt aaccgtgtccc agatgttcatgtt caa 453

<210> 309

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 309

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gin Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120

WO 2005/037989

PCT/US2003/024918

49076.000004pct2.10.207.655 Seq List Text 07.24.03.txt
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln
145 150

<210> 310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for engineering 14 amino acids from
IgA-T4

<400> 310
gttgttgcac agccagttcc ctcaactcca cctaccat ctccttcaac t 51

<210> 311
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 311
atgggggtac tgctcacaca gaggacgctg ctcagtctgg tccttgact cctgtttcca 60
acatggcga gcatg 75

<210> 312
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 312
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met 20

<210> 313
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 313
gcaatgcacg tggcccaqcc tgcgtgtggta ctggccagca gccgaggcat cgccagctt 60
gtgtgtgagat atgcacatcc aggcaaaagcc actgaggatcc gggtgacagt gcttcggcag 120
gctgacagcc aggtgactga agtctgtgcg gcaacctaca tgacggggaa tgatgttggac 180
ttcccttagatg attccatctg cacggggcacc tccagtgaa atcaagtgaa cttcaactatc 240
caaggactga gggccatggaa cacgggactc tacatctgca aggttgagatc catgtacc 300
ccggccatact acctgggcat aggcaacggaa acccagattt atgttaattga tccagaaccg 360
tgccggattt ct 372

<210> 314
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<400> 314

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
 1 5 10 15
 Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
 20 25 30
 Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
 35 40 45
 Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp
 50 55 60
 Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
 65 70 75 80
 Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
 85 90 95
 Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
 100 105 110
 Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 115 120

<210> 315

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 315

atgggggtac tgctcacaca gaggacgctg ctcagttcg tccttgcact cctgttcca 60
 agcatggcga tgcatggcaat gacgtggcc cagctgtcg tggtaactggc cagcagccg 120
 ggcatcgcca gctttgtgtg ttggatgtca ttcggggcc aaggccatgg ggtccgggtg 180
 acagtgcctc ggccggctga caggcagggt actggaaatc gtgcggcaac ctacatgtat 240
 gggaaatggat tgaccatccat agatgattcc attcgtcccg gacacctcccg tggaaatcgat 300
 gtgaaacctca ctatccaaagg atcgaggccc atggacacccg gactctatcat ctgcgaagg 360
 gagttccatgg atcccccccgcat atactatccgt ggcataggcc accggaaacccca gattttatgtt 420
 atttgatcccg aaccgtggcc agatccatgtat caaacccaaaat ttcttgacaa aactccacaca 480
 tccccccaccgt cccccggccat tgaacttcccg tggggatgtcg cagttttccct ctccccccca 540
 aaacccaaagg acacccctcat gatctcccg accccctgggg tcatatgcgt ggttgtggac 600
 gtgagccacg aagacccctga ggtcaatgcg actggatcg tggacggcg gggatgtcat 660
 aaatggcaaga caaaccccgcc ggaaaggccat tacaatgcgt tgatccgttg yttatgtcg 720
 ctccatccgtcc tgccacccggat ctgggtgaat gcaaggatg acaaatgtcaa gttttcccaat 780
 aaaggccctcc cagccccccat cgaaaaaaaca atctccaaagg cc当地ggggcc gcccggggaa 840
 ccacagggtgt acacccctcc cccatcccg gatggatcg tcaagaacca gttcagctgg 900
 acctggcttgc tcaaaaggctt ctatccatgcg gacatcccg tggatgtggg gagaatgggg 960
 cggccggaga aacaaatccat gacccggct cccgggtctg actccacccgg ctcccttc 1020
 ctccatccatgcg agctccacccgg tggacaaatgcg agggtggccg aggggaaatcg ctatccatgcg 1080
 tccctgtatgcg atggatccgtt gcacacccat tacaatgcgt agatgccttc cctgtctccg 1140
 ggatggatgtat 1149

<210> 316

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 316

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr 115 120 125
 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Gly 130 135 140
 Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Ser Asp Lys Thr His Thr 145 150 155 160
 Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe 165 170 175
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 180 185 190
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 195 200 205
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 210 215 220
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 225 230 235 240
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 245 250 255
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 260 265 270
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro 275 280 285
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val 290 295 300
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 305 310 315 320
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp 325 330 335
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp 340 345 350
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 355 360 365
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 370 375 380

<210> 317

<211> 1221

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 317

atgggggtac tgcgcacaca gaggacgctg ctcagtcgg tcccttgcaact cctgtttcca 60
 agcatggcga gcatggcaat gcacgtggcc cagccgtcg tggtactggc cagcagccga 120
 ggatccgcga gcttigtgtq tgatgtatgc tcctccaggca aagccactga ggttccggtg 180
 acagtgcgtc ggcaggcgtga caqccagggtg actgaagtct gtgcggcaac ctacatgtatgc 240
 gggaaatgtgt tgaccttctt agatgtatcc atclgcacgg gacccctccag tggaaatcaa 300
 gtqaaccctca ctatccaaagg atcgaggccc atggacacgg gactctatacl ctgcgaagggt 360
 gagetcatgtt atccacccgt atactaccgtg ggcataggca acggaaacctca gatttatgtta 420
 attgtatccag aacctgtccc agatgttgcgat ctcggcaggct ctcactactcc accatccccca 480
 tcicccctcaat ctccacccatc cccatctcc tcatgtctggc acccccggactc gtactgtc 540
 cgacccggccc tgaggagact gctcttaggt tcagaagcgta tccctacgtg caactgtacc 600
 ggccctggggat atgtccctagg tgtcacccctt acctggacgc ctccaaatgg gaagacgtc 660
 gttaaaggac cacctggccg tgacccctgtt ggctgttaca ggctgttccag tggcttcggc 720
 ggctgtccggc agccatggaaat cccttacttca acatccactt gactgttgc ctaccccgac 780
 tccaaggaccc cgtcaatccgc cacccttca aatcccgaa acacatccgc gccccggatc 840
 caccctgtcg cggccggccg ggaggactg cggcttcggc acgtctggtgac gctgcacgtc 900
 ctggcaggctg gtttcggccccc aaaggatgtg ctgttgcgtt gctgtcagggg gtcaacaggag 960
 ctggcccccggc agaaatgtttt gactgtggca tccggcagg aaccccaacca gggcaccac 1020
 accttcgtcg gtagccatcatc actgcgcgtg gcaaggccggd actggaaagaa gggggacacc 1080
 ttctctgtca tgggtggccca cgaggccctt cgtctggccct tcacacagaa gaccatcgac 1140
 cgcttggcggtt gtaaaaccatc ccatgttcaat gttgttcgttgc tcatggccga gttggacggc 1200

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
acctgctact gataatctag a

1221

<210> 318
<211> 403
<212> PRT
<213> Artificial Sequence<220>
<223> fusion polypeptide<400> 318
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
145 150 155 160
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
165 170 175
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
180 185 190
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
195 200 205
Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro
210 215 220
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
225 230 235 240
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
245 250 255
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser
260 265 270
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu
275 280 285
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
290 295 300
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
305 310 315 320
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
325 330 335
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
340 345 350
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
355 360 365
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
370 375 380
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly
385 390 395 400
Thr Cys Tyr<210> 319
<211> 1209
<212> DNA
<213> Artificial Sequence

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 319

atgggggtac tgctcacaca gaggacgctg ctcagttctgg tccttgcact cctgtttcca 60
 agcattgcga gcatggcaat gcacgtggcc cagccgtcg tggtaactgc cagcagccga 120
 ggcatcgcca gccttgtgtg tgagatgfga ttcccggca aqccactga ggtccgggtg 180
 acatgtctt cgccggctga cagccgggtg atcgaatgtc gtccggcaac ctatcatgtg 240
 gggaaatgagt tgacccttcat agatgttcc atctgcacgg gcaccctccag tggaaatcca 300
 gtgaacccca ctatccaaagc atctggggcc atggacacgg gacttcatat ctgcggatgtg 360
 gagctcatgt accccccccg atactacccgt ggcatggca acggaaacca gattttatgtg 420
 attgtatccca aaccgtggcc agatgttgcgt cccatccatc accttacccca 480
 tctccctca caatccatc cccatccatc tcatgtgcg acccccccact gtcatgcac 540
 cgacccggcc tcggggactt gctttaggt tcagaaggca tccttcacgtg cacactgacc 600
 ggccctgagag atgcgttcagg tgatccatc acctggacca cctcaatgtg gaagagcgct 660
 gttcggatgg caccctggcg tgacccctgtg gctgtcatac gcgtgttcag tgcttcgtccg 720
 ggctgtccg agccatggaa ccatggggaa ctatccatc gcactgtctc ctatccccggag 780
 tccaaagcccg cgcgttacccg cacccttcga aaatccggaa acacatccg gccggagggt 840
 caccctgtcg cgccggccgc ggaggagctg gcccgttgcggc acgttggatgc octgtacgtc 900
 ctggcgcgtg gcttcagcccc caaaggatgtg ctgggttgcgt ggctgcgggg gtccacaaagd 960
 ctggcccccggc agaaatgttcc gatctggccat ccccgccagg acgttggacca gggcaccacc 1020
 acctccgtcg tgaccatgt actcggcggtg gcaggccgggg actggaaagaa ggggacccatc 1080
 ttctccgtca tggtggccca cgaggccctg ccggctggccct tcacacaaagaa gaccatcgac 1140
 cgcgttgcgg gtaaaaccac ctatgtcaat tgctgttg tcatggggaa gggtggactgt 1200
 taatctgtaa 1209

<210> 320

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 320

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125
 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
 145 150 155 160
 Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
 165 170 175
 Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
 180 185 190
 Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
 195 200 205
 Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro
 210 215 220
 Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
 225 230 235 240
 Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
 245 250 255
 Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
 275 280 285
 Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
 290 295 300
 Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
 305 310 315 320
 Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
 325 330 335
 Gln Gly Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
 340 345 350
 Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
 355 360 365
 Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
 370 375 380
 Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
 385 390 395

<210> 321
<211> 328
<212> DNA
<213> Artificial sequence

<220>
<223> fusion polynucleotide

<400> 321
 cctgaactcc tggggggatc gtcagtttc ctcttcccc caaaaccaa ggacaccctc 60
 atgatctccc ggacccctga ggtcacatgc gtgtgtgtgg acgtgaggcc caaaaaaggcc 120
 gaggtcaagt tcaactggta cttggacggc gtggaggatgc ataatggccaa gacaaaaggcc 180
 cggggaggcc agtacaacag cactgacccgt gtggtcagcc tcctccacgt ctcgcaccc 240
 gacttgtcta atggcaaga gtcatacgatc aagggttccaa acaaaggccct cccaggcccc 300
 atcgagaaaa ccatctccaa agccaaag 328

<210> 322
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 322
 Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
 1 5 10 15
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 20 25 30
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 35 40 45
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 50 55 60
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 65 70 75 80
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 85 90 95
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105

<210> 323
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acids surrounding the proline at 238

<400> 323

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser	1 5 10
---	--

<210> 324
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid substitution of Serine for Proline at 238

<400> 324
Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
1 5 10

<210> 325
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to PCR IgE Fc

<400> 325
gttggatc acgtctgctc cagggacttc accccc

<210> 326	35
-----------	----

<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to PCR IgE Fc

<400> 326
gttggttcta gattaacttt taccgggatt tacagacacc gctcgctgg

<210> 327	49
-----------	----

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligo to provide open reading frame at carboxy end of CH₄ to read into transmembrane and cytoplasmic tail of another protein

<400> 327
gttggtttcg aaggatccgc tttaccggga ttacagaca ccgctcgctg g

<210> 327	51
-----------	----

<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 328
tgatcacgtc tgctccaggg acttcacccc gcccaccgtg aagatcttac agtcgtccctg 60
cgccggccg gggcaactcc ccccgaccat ccaacgtccctg tgccctcgctc ctgggttacac 120
ccccggact atcaacatca cctggctgaa ggacggccggat gtcatggacg tgatgttc 180
caccggccctt accacgcggg agggtgaaact ggccctccaca caaaaggcgagc tcacccctcag 240
ccagaacgtc ttggctgtcgg accgcaccaata caccgtccggat gtacacatc aagggttacac 300
ttttggggac agcacaacaatc agtgtgcaga ttccaaacccgg agaggggtgaa gccccttac 360
aaggccggccc agcccggttcg acgttgttcat ccccaactggatc cccacgtacat cctgtctgtt 420

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ggtggacctg gcaccaggca agggggacgt gaacctgacc tggtcccgaa ccagtggaa 480
 gcccgtgaac cacttcacca gaaaggagga gaagcagcgc aatggcagct taaccgtc 540
 gtcacccctg ccgggtggca cccgagactg atggaggggg gagaccttac atgtcagggt 600
 gaccacccctt cacttgcggca gggccctcat gggttccacg accaaagacca ggccccccgg 660
 tgctgcggccgaa gaagtctatg cggttgcgac gccggatgg ccggggagcc ggacacaacgg 720
 cacccctcgcc tgccgtatcc agaaatctcat gctcgaggac attcctgggtc agtgtgtcga 780
 caacgagggtg acgtctcccgac acgccccggca cagcagcagc cagccccggca agaccaaagg 840
 ctccggcttc ttccgtttca gcccctggca ggtgaccagg gccgaatgg agcagaagaaga 900
 tgagttatcatc tgccgtcgag tccatgaggc aagcagggccc tcacagaccc tccacgcgac 960
 ggtgttgcata aatccggta aagcgatcc ttccga 996

<210> 329

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 329

Asp	His	Val	Cys	Ser	Arg	Asp	Phe	Thr	Pro	Pro	Thr	Val	Lys	Ile	Leu
1									10				15		
Gln	Ser	Ser	Cys	Asp	Gly	Gly	Gly	His	Phe	Pro	Pro	Thr	Ile	Gln	Leu
								20					25		
Leu	Cys	Leu	Val	Ser	Gly	Tyr	Thr	Pro	Gly	Thr	Ile	Asn	Ile	Thr	Trp
								35				40		45	
Leu	Glu	Asp	Gly	Gln	Val	Met	Asp	Val	Asp	Leu	Ser	Thr	Ala	Ser	Thr
						50						55		60	
Thr	Gln	Glu	Gly	Glu	Leu	Ala	Ser	Thr	Gln	Ser	Glu	Leu	Thr	Leu	Ser
						65					70		75		80
Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr	Tyr	Thr	Cys	Glu	Val	Thr	Tyr
						85					90			95	
Gln	Gly	His	Thr	Phe	Glu	Asp	Ser	Thr	Lys	Lys	Cys	Ala	Asp	Ser	Asn
				100					105				110		
Pro	Arg	Gly	Val	Ser	Ala	Tyr	Leu	Ser	Arg	Pro	Ser	Pro	Phe	Asp	Leu
						115				120			125		
Phe	Ile	Arg	Lys	Ser	Pro	Thr	Ile	Thr	Cys	Leu	Val	Val	Asp	Leu	Ala
						130				135			140		
Pro	Ser	Lys	Gly	Thr	Val	Asn	Leu	Thr	Trp	Ser	Arg	Ala	Ser	Gly	Lys
						145				150			155		160
Pro	Val	Asn	His	Ser	Thr	Arg	Lys	Glu	Glu	Lys	Gln	Arg	Asn	Gly	Thr
						165				170			175		
Leu	Thr	Val	Thr	Ser	Thr	Leu	Pro	Val	Gly	Thr	Arg	Asp	Trp	Ile	Glu
						180				185			190		
Gly	Glu	Thr	Tyr	Gln	Cys	Arg	Val	Thr	His	Pro	His	Leu	Pro	Arg	Ala
						195				200			205		
Leu	Met	Arg	Ser	Thr	Thr	Lys	Thr	Ser	Gly	Pro	Arg	Ala	Ala	Pro	Glu
						210				215			220		
Val	Tyr	Ala	Phe	Ala	Thr	Pro	Glu	Trp	Pro	Gly	Ser	Arg	Asp	Lys	Arg
						225				230			235		240
Thr	Leu	Ala	Cys	Leu	Ile	Gln	Asn	Phe	Met	Pro	Glu	Asp	Ile	Ser	Val
						245				250			255		
Gln	Trp	Leu	His	Asn	Glu	Val	Gln	Leu	Pro	Asp	Ala	Arg	His	Ser	Thr
						260				265			270		
Thr	Gln	Pro	Arg	Lys	Thr	Lys	Gly	Ser	Gly	Phe	Phe	Val	Phe	Ser	Arg
						275				280			285		
Leu	Glu	Val	Thr	Arg	Ala	Glu	Trp	Glu	Gln	Lys	Asp	Glu	Phe	Ile	Cys
						290				295			300		
Arg	Ala	Val	His	Glu	Ala	Ala	Ser	Pro	Ser	Gln	Thr	Val	Gln	Arg	Ala
						305				310			315		320
Val	Ser	Val	Asn	Pro	Gly	Lys	Ala	Asp	Pro	Ser					
						325				330					

<210> 330

<211> 63

<212> DNA

<213> Artificial Sequence

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 334
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 334
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Val Val Ser Asp His Val Cys Ser Arg Asp
260 265 270
Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
275 280 285
Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
290 295 300
Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
305 310 315 320
Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
325 330 335
Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
340 345 350
Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
355 360 365
Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
370 375 380
Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
385 390 395 400
Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
405 410 415
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
420 425 430
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
435 440 445
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

450	455	460
Val	Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys	
465	470	475
Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro		480
485	490	495
Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln		
500	505	510
Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val		
515	520	525
Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys		
530	535	540
Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu		
545	550	555
Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala		560
565	570	575
Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys		
580	585	590

<210> 335

<211> 339

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 335

```
cagggtcage tgaaggaggc aggacctggc ctgggtcaac cgacacagac cctgtccctc 60
acatgcactg tctctgggtt ctcattaacc acgcgatgggt tacactggat tcgacgacct 120
ccggaaagg gtcgtggatg gatggaaata atattatgt atggggccac agattataata 180
tcagcaata aatccagact gagcatcagc agggacacct ccaagagcca atgtttctta 240
aaaatcaaca gtcgtcaaac tgatgacaca gcgtatgtt actgtgtccag aatccactt 300
gattactggc gccaaggagt catggtcaca gtctccctct 339
```

<210> 336

<211> 321

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 336

```
gacattgtgc tcacttcagtc tccaaacaacc atagctgcatt ctcaggggaa gaaggtcacc 60
atcacctggc gtgcaggctc cagtgtaaatg tacatgtact ggtaaccggca gaagtcaggc 120
gcctcccccta aactctggat ttatgacaca tccaaaggctgg ctitctggatgt tccaaatcg 180
ttcagtgca gttgggtctgg gaccccttat ttcttcgc当地 tccaaacccatggaaactgaa 240
gtatgtgc当地 ttatctgt tcagcaggatgg agtagtactc cgctcacgtt cgggtctgg 300
accaaggctgg agatcaaaccg 321
```

<210> 337

<211> 785

<212> DNA

<213> Artificial sequence

<220>

<223> fusion polynucleotide

<400> 337

```
aagctttagt atttcaaatg gcagattttc agcttcctgc taatctgtgc ttcaatgtata 60
atgtcccgatg gagtcgacat tttgtctact cagtctccaa caaaccatagc tgatctccaa 120
ggggagaagg ctaccatcac ctggccgtcc agctcccaatgt taatgttacat gtatgtcc 180
cagcagaatg caggcccttc ccctaaactc ttgtatgtatg acacatccaa ctggcttctt 240
ggatgtccaa atgccttcag ttggcagtgg ttggggactt ctatctct cgcataacaa 300
accatggaga ctgaagatgc tgccactat tactgtcagc agtggtagat tactccgctc 360
```

See *Notes*, page 300.

WO 2005/037989

PCT/US2003/024918

<210> 338

211 1491

<212> DNA

<213> Artificial Sequence

<220>
<223>

<223> Fusion polynucleotide

<400> 338

<210> 339

<211> 1645

<212> DNA

<213> Artificial Sequence

220
223

22232 1031

<400> 339

atgtccatgc
tttttttttttt

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

<210> 340

<211> 1645

<212>

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 340

<210> 341

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 341

Gin Val Gin Leu Lys Glu Ala Gly Pro Gly Leu Val Gin Pro Thr Gin
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asp
 20 25 30
 Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile Lys
50 55 60
Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110
Ser

<210> 342
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 342
Asp Ile Val Leu Thr Gln Ser Pro Thr Thr Ile Ala Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Tyr Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Asn Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Ala Ile Asn Thr Met Glu Thr Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Leu Thr
85 90 95
Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 343
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 343
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
20 25 30
Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
35 40 45
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
50 55 60
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
65 70 75 80
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
85 90 95
Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
145 150 155 160
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
165 170 175
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
180 185 190
195 200 205
Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
210 215 220
Leu Lys Ile Asn Ser Ile Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
225 230 235 240
Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
245 250 255
Ser Ser

<210> 344
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 344
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
20 25 30
Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
35 40 45
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
50 55 60
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
65 70 75 80
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
85 90 95
Ile Asn Thr Met Gly Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
130 135 140
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
145 150 155 160
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
165 170 175
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
180 185 190
Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
195 200 205
Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
210 215 220
Leu Lys Ile Asn Ser Ile Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
225 230 235 240
Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
245 250 255
Ser Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
260 265 270
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
290 295 300
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 345
<211> 543
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 345
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ala Ser Pro Gly Glu Lys val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 260 265 270
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

WO 2005/037989

PCT/US2003/024918

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
 340 345 350
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser
 485 490 495
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile
 500 505 510
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu
 515 520 525
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 530 535 540

<210> 346

<211> 543

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 346

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Gly Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro

DOI: 10.1007/s00339-007-0301-1

WO 2005/037989

PCT/US2003/024918

```

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260          265          270
Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe
 275          280          285
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290          295          300
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305          310          315          320
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325          330          335
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340          345          350
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355          360          365
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370          375          380
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385          390          395          400
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405          410          415
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gin Pro
 420          425          430
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435          440          445
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450          455          460
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465          470          475          480
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser
 485          490          495
Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile
 500          505          510
Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu
 515          520          525
Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 530          535          540

```

<210> 347

<211> 1527

<212> DNA

<213> Artificial sequence

<220>

<<23> fusion polynucleotide

<400> 347
339ctt3±8

WO 2005/037989

PCT/US2003/024918

49076_000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

ggctcccttc tcctctacag caagcttacc gtggacaaga gcacgttgcgca gcaaggaaac 1440
gtcttctcat gctccgttat gcatggatct ctgcacaacc actacacgcga gaagagcctc 1500
tccctgtctc cgggttaatg atcttaga 1527

<210> 348
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 348
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly val Asp Ile Gln Met Thr Gln Thr Thr Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45
Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60
Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly
65 70 75 80
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95
Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110
Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Val
115 120 125
Thr Lys Arg Glu Leu Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ile Asp Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
145 150 155 160
Leu Val Lys Pro Gly Ala Ser Met Ser Cys Lys Ala Ser Gly Tyr Ser
165 170 175
Phe Thr Gly Tyr Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn
180 185 190
Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr
195 200 205
Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
210 215 220
Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala
225 230 235 240
Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr
245 250 255
Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Asp Gln
260 265 270
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
275 280 285
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
290 295 300
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305 310 315 320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
325 330 335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
340 345 350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
355 360 365
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
370 375 380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385 390 395 400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
405 410 415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
420 425 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
435 440 445

```

Digitized by srujanika@gmail.com

WO 2005/037989

PCT/US2003/024918

```

Lys Thr Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
450 455 460
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465 470 475 480
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Ly
485 490 495
Ser Leu Ser Leu Ser Pro Gly Lys
500

```

<210> 349
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 349

<210> 350
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 350
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

1 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
5 10 15
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr val Thr val ser Ser Asp Gln Ser Asn Ser Glu
260 265 270
Glu Ala Lys Lys Glu Glu Ala Lys Lys Glu Glu Ala Lys Lys Ser Asn
275 280 285
Ser Val Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr
290 295 300
Pro Gly Asp Arg Val Ser Leu Ser Ser Cys Arg Ala Ser Gln Ser Ile Ser
305 310 315 320
Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu
325 330 335
Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly Ile Pro Ser Arg Phe
340 345 350
Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser val
355 360 365
Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln His Gly His Ser Phe
370 375 380
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly
385 390 395 400
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gln Ile Gln
405 410 415
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Arg
420 425 430
Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Cys Arg Met Gln
435 440 445
Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile Gly Trp Ile
450 455 460
Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu Gln Gly Arg
465 470 475 480
Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
485 490 495
Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg Ser
500 505 510
Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp Gly Gln Gly
515 520 525
Thr Leu Val Thr val Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr
530 535 540
His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
545 550 555 560

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 565 570 575
 Thr Pro Glu Val Thr cys Val Val val Asp val Ser His Glu Asp Pro
 580 585 590
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 595 600 605
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 610 615 620
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 625 630 635 640
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 645 650 655
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 660 665 670
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 675 680 685
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 690 695 700
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 705 710 715 720
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 725 730 735
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 740 745 750
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 755 760 765

<210> 351

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 351

aagcttgcgc ccatggatt tcaagtgcag attttcgact tcctgtataat cagtgtttca 60
 gtcatataatg ccaggaggaca aatttgttctc tccccgtctc cagaatccct gtcgtgcattc 120
 ccaggggaga aggtcacatc gacttgcggac gccaggctaa gtgttaaggta catgcactgg 180
 taccaggcaga aaggccgatc ctcccccaa ccctggattt atgccttactc caacctggct 240
 tctggagatcc ctgtcgccctt cagtgccgtt gggctgggaa cctcttactc ttccaaactc 300
 agcCAGatgg aaggcttggaa tgctgcctacttattactggc agcagtggag tttaaaccctt 360
 cccacgtttc ggatctggac ccaggctggag ctggaaatggat ggcgggtgcctt gggcggctgg 420
 ggatctggag gaggttggggat ctctcaggct taatctacagc agtctggggc tgaggctgg 480
 aggccctgggg Ctcctggaa gatgttctt aaggcttcgtt gctacacattt taccaatgtt 540
 aatatgcact gggttaaaagca gacacccatgg aaggccctgg aatggatgg agcttatttt 600
 ccaggaaatgg gtgtatcttc ctacaaatcg aagttcaagg qcaaggccac actgtatgtt 660
 gacaaatccc ccaggacacgc ctatcatcgag cttagcggcc tgacatctga agatctcg 720
 gtcttatttc tgtaaggatc ggtgtatctat agtaactctt actgttactt ctgtatctgg 780
 ggcacaggaa ccacgggtcact ctgtcttcttc gatcgaggc ccaaatcttc tgacaaaact 840
 cacatcatccc cacgttcccccc acggacccatgat ctctctgggg gatcgicagt ctcccttc 900
 ccccaaaaaac ccaaggacac cttcatgtatcc tcccgaggacc ctgaggatCac atgcgtgtgg 960
 gtggacgtgtg gccaaggaaatgg cccgtggggat aagttcaactt ggtacgtggg Cggcgtggag 1020
 gtggatcaatgg ccaaggacaaa gcccgggggg gacgacgtaca acaggacgtt ccgttgttgg 1080
 agcgcttca ccgtccgtca ccaggactgg ctgtatgggg agggatcacaa gtgcgaatgtt 1140
 tccaaacaaa ccctcccaac ccccatcgag aaadaaatctt ccaaaaggccaa aggccggcc 1200
 cgagaaccaa aagggtatcacat cctyccccca tcccccggatg agctgtaccaaa gaaccggatc 1260
 aogctgtaccc gctctggatca aaggcttctat cccaggcgaca tcggccgtgg tggtggagage 1320
 aatggggcagc cggagaaatcaatcaaggacc acggcccttccg tgctggatcc cgacggcttc 1380
 ttcttcctct acacgttccatgg cccatgtgg aagactggatgg ggcaggagg gaaacgttcc 1440
 tcatgttcccg tgatgtatggatgg cccatgtgg aaccaactataa cgcagaaag gcttcctccgt 1500
 tctccgggtta aatgtatcgat a

<210> 352

<211> 500

<212> PRT

<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<220> fusion polypeptide
<400> 352
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
260 265 270
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340 345 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

WO 2005/037989

PCT/US2003/02498

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 353

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 353

atggctgtct tggggctgct cttctgcctg gtgacatttc caagctgtgt cctatcccg 60
gtgcagtcga aqcaqtcagg acctggccta gtgcagtcct cacagagctt gtcacatccc 120
tgccacatgt ctgggttctt attaaactcc tatgtgtac actgggttgc ccagtctcc 180
ggaaagggtc tggagggtct gggagggtata tgtaggtgtt gaaatcacaataatgtca 240
gctttcatat ccagactgtg carccccaag gacgattccaa agagccaaat tttttttaaa 300
atgaaacatgc tgcacactaa tgacacaggc atttattact tgcccgaaaa tgggggtgtat 360
aactaccctt attactatgc tatggacta tggggtcaga gacccctcgtt caccgttcc 420
tca 423

<210> 354

<211> 366

<212> DNA

<213> qArtificial Sequence

<220>

<223> fusion polynucleotide

<400> 354

cagggtcagc tgaaggcgtc aggacctggc ctatgtcgtt ctcacagag cctgtccatc 60
acctgtcagc ttctctgttt ctatcaaactt acatctgtt tacactgggtt tgcgcgtttc 120
ccggaaaacgg gtcgtggatgtt gtcggggatgtt atatggatgtt gtggaaatcac agactataat 180
gcaggctttca tatccagactt gaggatcacc aaggacgtt ccagggccaa agttttttttt 240
aaaatgaaaca gtcgtcaacc taatgtacaca gccattttt actgtgtccatc aatgtgggtt 300
gataactacc ttatattacta tgctatggac factgggttca aaggaaacctc agtcaccgtc 360
tcctca 366

<210> 355

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 355

atggaggctt ctgtctcgt tctggggctg ctttgtctt ggatccctgg atccactgtca 60
gatatgttgc tgacgcggc tgcatctccaa aatccgtca ctcttggaaat atcagtc 120
atcccttcgtt ggtcttagtaa ggtcttcata catatgtt gcatcactta ttgttatgg 180
tatctgtcaga aggcagggtca gttcttcgtt ccctgttattt atcagatgtc caacccgttcc 240
tcaggatgttcc cagacagggtt ctagtgcgtt gggtcggaa ctgtatttccatc actgtgttcc 300
agcaggatgtt aggtgtggaa tgtaggtgtt tattactgtt ctcaaatctt agaaacttcc 360
ctcacgttcg gtgtgtggac caagctggat ctgtaaacgg 399

<210> 356

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 356

aaacctggcc ccatgagggtt ctctgtcgtt cttctggggc tgcttgcgtt ctggatccct 60
ggatccatgtt ctagatgtt gatgtacgttgc gtcgttccatctt ccacatccgtt cactcttggaa 120
acatcgttcc ccatcttcgtt caggttgcgtt aagatgttccatc tcatatgtt tgccatcact 180
tattttgtttt ggtatgtcga aaggttcggc cagtttccttc acgttccgtt atatccatgtt 240
tccaaacctt ccttcagggtt cccagacagggtt cttatgttgcgtt gttgggttccatc aactgttcc 300
acactgtggaa tcagtcgttgg ggggtgttgcgtt tttttttttt tttttttttt tttttttttt 360
cttagaaacctt cgttcacgtt cttatgttgcgtt accaaatgttgcgtt aactgtgttcc 420